

AP20 Rec'd PCT/PTO 23 JUN 2006

SEQUENCE LISTING

<110> Kinch, Michael S.

<120> EphA2 VACCINES

<130> 10271-148-999

<140>

<141>

<150> US 60/532,696

<151> 2003-12-24

<150> US 60/602,588

<151> 2004-08-18

<150> US 60/615,548

<151> 2004-10-01

<150> US 60/617,564

<151> 2004-10-07

<160> 72

<170> PatentIn version 3.2

<210> 1

<211> 3963

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (138)..(3068)

<400> 1

attaaggact cggggcagga ggggcagaag ttgcgcgcag gccggcgggc gggagcggac 60

accgaggccg gcgtgcaggc gtgcgggtgt gcgggagccg ggctcggggg gatcggaccg 120

agagcgagaa gcgcggc atg gag ctc cag gca gcc cgc gcc tgc ttc gcc 170

Met Glu Leu Gln Ala Ala Arg Ala Cys Phe Ala
1 5 10

ctg ctg tgg ggc tgt gcg ctg gcc gcg gcc gcg gcg cag ggc aag 218

Leu Leu Trp Gly Cys Ala Leu Ala Ala Ala Ala Ala Ala Gln Gly Lys
15 20 25

gaa gtg gta ctg ctg gac ttt gct gca gct gga ggg gag ctc ggc tgg 266

Glu Val Val Leu Leu Asp Phe Ala Ala Ala Gly Gly Glu Leu Gly Trp
30 35 40

ctc aca cac ccg tat ggc aaa ggg tgg gac ctg atg cag aac atc atg 314

Leu Thr His Pro Tyr Gly Lys Gly Trp Asp Leu Met Gln Asn Ile Met
45 50 55

aat gac atg ccg atc tac atg tac tcc gtg tgc aac gtg atg tct ggc 362

Asn Asp Met Pro Ile Tyr Met Tyr Ser Val Cys Asn Val Met Ser Gly
60 65 70 75

gac cag gac aac tgg ctc cgc acc aac tgg gtg tac cga gga gag gct Asp Gln Asp Asn Trp Leu Arg Thr Asn Trp Val Tyr Arg Gly Glu Ala 80 85 90	410
gag cgt atc ttc att gag ctc aag ttt act gta cgt gac tgc aac agc Glu Arg Ile Phe Ile Glu Leu Lys Phe Thr Val Arg Asp Cys Asn Ser 95 100 105	458
ttc cct ggt ggc gcc agc tcc tgc aag gag act ttc aac ctc tac tat Phe Pro Gly Ala Ser Ser Cys Lys Glu Thr Phe Asn Leu Tyr Tyr 110 115 120	506
gcc gag tgc gac ctg gac tac ggc acc aac ttc cag aag cgc ctg ttc Ala Glu Ser Asp Leu Asp Tyr Gly Thr Asn Phe Gln Lys Arg Leu Phe 125 130 135	554
acc aag att gac acc att gcg ccc gat gag atc acc gtc agc agc gac Thr Lys Ile Asp Thr Ile Ala Pro Asp Glu Ile Thr Val Ser Ser Asp 140 145 150 155	602
ttc gag gca cgc cac gtg aag ctg aac gtg gag gag cgc tcc gtg ggg Phe Glu Ala Arg His Val Lys Leu Asn Val Glu Glu Arg Ser Val Gly 160 165 170	650
ccg ctc acc cgc aaa ggc ttc tac ctg gcc ttc cag gat atc ggt gcc Pro Leu Thr Arg Lys Gly Phe Tyr Leu Ala Phe Gln Asp Ile Gly Ala 175 180 185	698
tgt gtg gcg ctg ctc tcc gtc cgt gtc tac tac aag aag tgc ccc gag Cys Val Ala Leu Leu Ser Val Arg Val Tyr Tyr Lys Lys Cys Pro Glu 190 195 200	746
ctg ctg cag ggc ctg gcc cac ttc cct gag acc atc gcc ggc tct gat Leu Leu Gln Gly Leu Ala His Phe Pro Glu Thr Ile Ala Gly Ser Asp 205 210 215	794
gca cct tcc ctg gcc act gtg gcc ggc acc tgt gtg gac cat gcc gtg Ala Pro Ser Leu Ala Thr Val Ala Gly Thr Cys Val Asp His Ala Val 220 225 230 235	842
gtg cca ccg ggg ggt gaa gag ccc cgt atg cac tgt gca gtg gat ggc Val Pro Pro Gly Gly Glu Glu Pro Arg Met His Cys Ala Val Asp Gly 240 245 250	890
gag tgg ctg gtg ccc att ggg cag tgc ctg tgc cag gca ggc tac gag Glu Trp Leu Val Pro Ile Gly Gln Cys Leu Cys Gln Ala Gly Tyr Glu 255 260 265	938
aag gtg gag gat gcc tgc cag gcc tgc tcg cct gga ttt ttt aag ttt Lys Val Glu Asp Ala Cys Gln Ala Cys Ser Pro Gly Phe Phe Lys Phe 270 275 280	986
gag gca tct gag agc ccc tgc ttg gag tgc cct gag cac acg ctg cca Glu Ala Ser Glu Ser Pro Cys Leu Glu Cys Pro Glu His Thr Leu Pro 285 290 295	1034
tcc cct gag ggt gcc acc tcc tgc gag tgt gag gaa ggc ttc ttc cgg Ser Pro Glu Gly Ala Thr Ser Cys Glu Cys Glu Glu Gly Phe Phe Arg 300 305 310 315	1082

gca cct cag gac cca gcg tcg atg cct tgc aca cga ccc ccc tcc gcc Ala Pro Gln Asp Pro Ala Ser Met Pro Cys Thr Arg Pro Pro Ser Ala 320 325 330	1130
cca cac tac ctc aca gcc gtg ggc atg ggt gcc aag gtg gag ctg cgc Pro His Tyr Leu Thr Ala Val Gly Met Gly Ala Lys Val Glu Leu Arg 335 340 345	1178
tgg acg ccc cct cag gac agc ggg ggc cgc gag gac att gtc tac agc Trp Thr Pro Pro Gln Asp Ser Gly Gly Arg Glu Asp Ile Val Tyr Ser 350 355 360	1226
gtc acc tgc gaa cag tgc tgg ccc gag tct ggg gaa tgc ggg ccg tgt Val Thr Cys Glu Gln Cys Trp Pro Glu Ser Gly Glu Cys Gly Pro Cys 365 370 375	1274
gag gcc agt gtg cgc tac tcg gag cct cct cac gga ctg acc cgc acc Glu Ala Ser Val Arg Tyr Ser Glu Pro Pro His Gly Leu Thr Arg Thr 380 385 390 395	1322
agt gtg aca gtg agc gac ctg gag ccc cac atg aac tac acc ttc acc Ser Val Thr Val Ser Asp Leu Glu Pro His Met Asn Tyr Thr Phe Thr 400 405 410	1370
gtg gag gcc cgc aat ggc gtc tca ggc ctg gta acc agc cgc agc ttc Val Glu Ala Arg Asn Gly Val Ser Gly Leu Val Thr Ser Arg Ser Phe 415 420 425	1418
cgt act gcc agt gtc agc atc aac cag aca gag ccc ccc aag gtg agg Arg Thr Ala Ser Val Ser Ile Asn Gln Thr Glu Pro Pro Lys Val Arg 430 435 440	1466
ctg gag ggc cgc agc acc acc tcg ctt agc gtc tcc tgg agc atc ccc Leu Glu Gly Arg Ser Thr Thr Ser Leu Ser Val Ser Trp Ser Ile Pro 445 450 455	1514
ccg ccg cag cag agc cga gtg tgg aag tac gag gtc act tac cgc aag Pro Pro Gln Gln Ser Arg Val Trp Lys Tyr Glu Val Thr Tyr Arg Lys 460 465 470 475	1562
aag gga gac tcc aac agc tac aat gtg cgc cgc acc gag ggt ttc tcc Lys Gly Asp Ser Asn Ser Tyr Asn Val Arg Arg Thr Glu Gly Phe Ser 480 485 490	1610
gtg acc ctg gac gac ctg gcc cca gac acc acc tac ctg gtc cag gtg Val Thr Leu Asp Asp Leu Ala Pro Asp Thr Thr Tyr Leu Val Gln Val 495 500 505	1658
cag gca ctg acg cag gag ggc cag ggg gcc ggc agc aag gtg cac gaa Gln Ala Leu Thr Gln Glu Gly Gln Gly Ala Gly Ser Lys Val His Glu 510 515 520	1706
ttc cag acg ctg tcc ccg gag gga tct ggc aac ttg gcg gtg att ggc Phe Gln Thr Leu Ser Pro Glu Gly Ser Gly Asn Leu Ala Val Ile Gly 525 530 535	1754
ggc gtg gct gtc ggt gtg gtc ctg ctt ctg gtg ctg gca gga gtt ggc Gly Val Ala Val Gly Val Val Leu Leu Leu Val Leu Ala Gly Val Gly 540 545 550 555	1802
ttc ttt atc cac cgc agg agg aag aac cag cgt gcc cgc cag tcc ccg	1850

Phe	Phe	Ile	His	Arg	Arg	Arg	Lys	Asn	Gln	Arg	Ala	Arg	Gln	Ser	Pro	
				560					565					570		
gag	gac	gtt	tac	ttc	tcc	aag	tca	gaa	caa	ctg	aag	ccc	ctg	aag	aca	1898
Glu	Asp	Val	Tyr	Phe	Ser	Lys	Ser	Glu	Gln	Leu	Lys	Pro	Leu	Lys	Thr	
			575					580					585			
tac	gtg	gac	ccc	cac	aca	tat	gag	gac	ccc	aac	cag	gct	gtg	ttg	aag	1946
Tyr	Val	Asp	Pro	His	Thr	Tyr	Glu	Asp	Pro	Asn	Gln	Ala	Val	Leu	Lys	
			590				595					600				
ttc	act	acc	gag	atc	cat	cca	tcc	tgt	gtc	act	cgg	cag	aag	gtg	atc	1994
Phe	Thr	Thr	Glu	Ile	His	Pro	Ser	Cys	Val	Thr	Arg	Gln	Lys	Val	Ile	
	605					610					615					
gga	gca	gga	gag	ttt	ggg	gag	gtg	tac	aag	ggc	atg	ctg	aag	aca	tcc	2042
Gly	Ala	Gly	Glu	Phe	Gly	Glu	Val	Tyr	Lys	Gly	Met	Leu	Lys	Thr	Ser	
	620				625					630					635	
tcg	ggg	aag	aag	gag	gtg	ccg	gtg	gcc	atc	aag	acg	ctg	aaa	gcc	ggc	2090
Ser	Gly	Lys	Lys	Glu	Val	Pro	Val	Ala	Ile	Lys	Thr	Leu	Lys	Ala	Gly	
				640					645					650		
tac	aca	gag	aag	cag	cga	gtg	gac	ttc	ctc	ggc	gag	gcc	ggc	atc	atg	2138
Tyr	Thr	Glu	Lys	Gln	Arg	Val	Asp	Phe	Leu	Gly	Glu	Ala	Gly	Ile	Met	
			655					660					665			
ggc	cag	ttc	agc	cac	cac	aac	atc	atc	cgc	cta	gag	ggc	gtc	atc	tcc	2186
Gly	Gln	Phe	Ser	His	His	Asn	Ile	Ile	Arg	Leu	Glu	Gly	Val	Ile	Ser	
		670					675					680				
aaa	tac	aag	ccc	atg	atg	atc	atc	act	gag	tac	atg	gag	aat	ggg	gcc	2234
Lys	Tyr	Lys	Pro	Met	Met	Ile	Ile	Thr	Glu	Tyr	Met	Glu	Asn	Gly	Ala	
	685					690					695					
ctg	gac	aag	ttc	ctt	cgg	gag	aag	gat	ggc	gag	ttc	agc	gtg	ctg	cag	2282
Leu	Asp	Lys	Phe	Leu	Arg	Glu	Lys	Asp	Gly	Glu	Phe	Ser	Val	Leu	Gln	
	700				705				710						715	
ctg	gtg	ggc	atg	ctg	cgg	ggc	atc	gca	gct	ggc	atg	aag	tac	ctg	gcc	2330
Leu	Val	Gly	Met	Leu	Arg	Gly	Ile	Ala	Ala	Gly	Met	Lys	Tyr	Leu	Ala	
				720					725					730		
aac	atg	aac	tat	gtg	cac	cgt	gac	ctg	gct	gcc	cgc	aac	atc	ctc	gtc	2378
Asn	Met	Asn	Tyr	Val	His	Arg	Asp	Leu	Ala	Ala	Arg	Asn	Ile	Leu	Val	
			735					740					745			
aac	agc	aac	ctg	gtc	tgc	aag	gtg	tct	gac	ttt	ggc	ctg	tcc	cgc	gtg	2426
Asn	Ser	Asn	Leu	Val	Cys	Lys	Val	Ser	Asp	Phe	Gly	Leu	Ser	Arg	Val	
		750					755					760				
ctg	gag	gac	gac	ccc	gag	gcc	acc	tac	acc	acc	agt	ggc	ggc	aag	atc	2474
Leu	Glu	Asp	Asp	Pro	Glu	Ala	Thr	Tyr	Thr	Thr	Ser	Gly	Gly	Lys	Ile	
	765					770					775					
ccc	atc	cgc	tgg	acc	gcc	ccg	gag	gcc	att	tcc	tac	cgg	aag	ttc	acc	2522
Pro	Ile	Arg	Trp	Thr	Ala	Pro	Glu	Ala	Ile	Ser	Tyr	Arg	Lys	Phe	Thr	
	780				785					790					795	
tct	gcc	agc	gac	gtg	tgg	agc	ttt	ggc	att	gtc	atg	tgg	gag	gtg	atg	2570
Ser	Ala	Ser	Asp	Val	Trp	Ser	Phe	Gly	Ile	Val	Met	Trp	Glu	Val	Met	

800	805	810	
acc tat ggc gag cgg ccc tac tgg	gag ttg tcc aac cac gag gtg atg		2618
Thr Tyr Gly Glu Arg Pro Tyr Trp	Glu Leu Ser Asn His Glu Val Met		
815	820	825	
aaa gcc atc aat gat ggc ttc cgg	ctc ccc aca ccc atg gac tgc ccc		2666
Lys Ala Ile Asn Asp Gly Phe Arg	Leu Pro Thr Pro Met Asp Cys Pro		
830	835	840	
tcc gcc atc tac cag ctc atg atg	cag tgc tgg cag cag gag cgt gcc		2714
Ser Ala Ile Tyr Gln Leu Met Met	Gln Cys Trp Gln Gln Glu Arg Ala		
845	850	855	
cgc cgc ccc aag ttc gct gac atc	gtc agc atc ctg gac aag ctc att		2762
Arg Arg Pro Lys Phe Ala Asp Ile	Val Ser Ile Leu Asp Lys Leu Ile		
860	865	870	875
cgt gcc cct gac tcc ctc aag acc	ctg gct gac ttt gac ccc cgc gtg		2810
Arg Ala Pro Asp Ser Leu Lys Thr	Leu Ala Asp Phe Asp Pro Arg Val		
880	885	890	
tct atc cgg ctc ccc agc acg agc	ggc tgc gag ggg gtg ccc ttc cgc		2858
Ser Ile Arg Leu Pro Ser Thr Ser	Gly Ser Glu Gly Val Pro Phe Arg		
895	900	905	
acg gtg tcc gag tgg ctg gag tcc	atc aag atg cag cag tat acg gag		2906
Thr Val Ser Glu Trp Leu Glu Ser	Ile Lys Met Gln Gln Tyr Thr Glu		
910	915	920	
cac ttc atg gcg gcc ggc tac act	gcc atc gag aag gtg gtg cag atg		2954
His Phe Met Ala Ala Gly Tyr Thr	Ala Ile Glu Lys Val Val Gln Met		
925	930	935	
acc aac gac gac atc aag agg att	ggg gtg cgg ctg ccc ggc cac cag		3002
Thr Asn Asp Asp Ile Lys Arg Ile	Gly Val Arg Leu Pro Gly His Gln		
940	945	950	955
aag cgc atc gcc tac agc ctg ctg	gga ctc aag gac cag gtg aac act		3050
Lys Arg Ile Ala Tyr Ser Leu Leu	Gly Leu Lys Asp Gln Val Asn Thr		
960	965	970	
gtg ggg atc ccc atc tga gcctcgacag	ggcctggagc cccatcggcc		3098
Val Gly Ile Pro Ile			
975			
aagaatactt gaagaaacag agtggcctcc	ctgctgtgcc atgctgggcc actggggact		3158
ttattttattt ctagttcttt cctccccctg	caacttccgc tgaggggtct cggatgacac		3218
cctggcctga actgaggaga tgaccaggga	tgctgggctg ggccctcttt ccctgcgaga		3278
cgcacacagc tgagcactta gcaggcaccg	ccacgtccca gcatccctgg agcaggagcc		3338
ccgccacagc cttcggacag acatatagga	tattcccaag ccgaccttcc ctccgccttc		3398
tcccacatga ggccatctca ggagatggag	ggcttgcccc agcgccaagt aaacagggtg		3458
cctcaagccc catttctctca cactaagagg	gcagactgtg aacttgactg ggtgagaccc		3518
aaagcgggtcc ctgtccctct agtgccttct	ttagaccctc gggcccatc ctcatccctg		3578

actggccaaa cccttgcttt cctgggcctt tgcaagatgc ttggttgtgt tgaggttttt 3638
 aaatatatat ttgtacttt gtggagagaa tgtgtgtgtg tggcaggggg ccccgccagg 3698
 gctggggaca gaggggtgtca aacattcgtg agctggggac tcagggaccg gtgctgcagg 3758
 agtgtcctgc ccatgccccca gtcggccccca tctctcatcc ttttggataa gtttctattc 3818
 tgtcagtgtt aaagattttg ttttgttga catttttttc gaatcttaat ttattatttt 3878
 ttttatattt attgttagaa aatgacttat ttctgctctg gaataaagtt gcagatgatt 3938
 caaacgaaa aaaaaaaaaa aaaaa 3963

<210> 2
 <211> 976
 <212> PRT
 <213> Homo sapiens

<400> 2

Met	Glu	Leu	Gln	Ala	Ala	Arg	Ala	Cys	Phe	Ala	Leu	Leu	Trp	Gly	Cys	
1				5					10					15		
Ala	Leu	Ala	Ala	Ala	Ala	Ala	Ala	Gln	Gly	Lys	Glu	Val	Val	Leu	Leu	
		20						25					30			
Asp	Phe	Ala	Ala	Ala	Gly	Gly	Glu	Leu	Gly	Trp	Leu	Thr	His	Pro	Tyr	
	35						40					45				
Gly	Lys	Gly	Trp	Asp	Leu	Met	Gln	Asn	Ile	Met	Asn	Asp	Met	Pro	Ile	
	50					55					60					
Tyr	Met	Tyr	Ser	Val	Cys	Asn	Val	Met	Ser	Gly	Asp	Gln	Asp	Asn	Trp	
65					70					75					80	
Leu	Arg	Thr	Asn	Trp	Val	Tyr	Arg	Gly	Glu	Ala	Glu	Arg	Ile	Phe	Ile	
			85						90					95		
Glu	Leu	Lys	Phe	Thr	Val	Arg	Asp	Cys	Asn	Ser	Phe	Pro	Gly	Gly	Ala	
			100					105					110			
Ser	Ser	Cys	Lys	Glu	Thr	Phe	Asn	Leu	Tyr	Tyr	Ala	Glu	Ser	Asp	Leu	
		115					120					125				
Asp	Tyr	Gly	Thr	Asn	Phe	Gln	Lys	Arg	Leu	Phe	Thr	Lys	Ile	Asp	Thr	
	130					135					140					
Ile	Ala	Pro	Asp	Glu	Ile	Thr	Val	Ser	Ser	Asp	Phe	Glu	Ala	Arg	His	
145					150					155					160	
Val	Lys	Leu	Asn	Val	Glu	Glu	Arg	Ser	Val	Gly	Pro	Leu	Thr	Arg	Lys	
			165						170					175		
Gly	Phe	Tyr	Leu	Ala	Phe	Gln	Asp	Ile	Gly	Ala	Cys	Val	Ala	Leu	Leu	
			180					185					190			
Ser	Val	Arg	Val	Tyr	Tyr	Lys	Lys	Cys	Pro	Glu	Leu	Leu	Gln	Gly	Leu	
		195					200					205				

Ala	His	Phe	Pro	Glu	Thr	Ile	Ala	Gly	Ser	Asp	Ala	Pro	Ser	Leu	Ala		
	210					215					220						
Thr	Val	Ala	Gly	Thr	Cys	Val	Asp	His	Ala	Val	Val	Pro	Pro	Gly	Gly		
225					230					235					240		
Glu	Glu	Pro	Arg	Met	His	Cys	Ala	Val	Asp	Gly	Glu	Trp	Leu	Val	Pro		
				245					250					255			
Ile	Gly	Gln	Cys	Leu	Cys	Gln	Ala	Gly	Tyr	Glu	Lys	Val	Glu	Asp	Ala		
			260					265					270				
Cys	Gln	Ala	Cys	Ser	Pro	Gly	Phe	Phe	Lys	Phe	Glu	Ala	Ser	Glu	Ser		
		275					280					285					
Pro	Cys	Leu	Glu	Cys	Pro	Glu	His	Thr	Leu	Pro	Ser	Pro	Glu	Gly	Ala		
	290					295					300						
Thr	Ser	Cys	Glu	Cys	Glu	Glu	Gly	Phe	Phe	Arg	Ala	Pro	Gln	Asp	Pro		
305					310					315					320		
Ala	Ser	Met	Pro	Cys	Thr	Arg	Pro	Pro	Ser	Ala	Pro	His	Tyr	Leu	Thr		
				325					330					335			
Ala	Val	Gly	Met	Gly	Ala	Lys	Val	Glu	Leu	Arg	Trp	Thr	Pro	Pro	Gln		
			340					345					350				
Asp	Ser	Gly	Gly	Arg	Glu	Asp	Ile	Val	Tyr	Ser	Val	Thr	Cys	Glu	Gln		
		355					360					365					
Cys	Trp	Pro	Glu	Ser	Gly	Glu	Cys	Gly	Pro	Cys	Glu	Ala	Ser	Val	Arg		
	370					375					380						
Tyr	Ser	Glu	Pro	Pro	His	Gly	Leu	Thr	Arg	Thr	Ser	Val	Thr	Val	Ser		
385					390					395					400		
Asp	Leu	Glu	Pro	His	Met	Asn	Tyr	Thr	Phe	Thr	Val	Glu	Ala	Arg	Asn		
				405					410					415			
Gly	Val	Ser	Gly	Leu	Val	Thr	Ser	Arg	Ser	Phe	Arg	Thr	Ala	Ser	Val		
			420					425					430				
Ser	Ile	Asn	Gln	Thr	Glu	Pro	Pro	Lys	Val	Arg	Leu	Glu	Gly	Arg	Ser		
	435					440					445						
Thr	Thr	Ser	Leu	Ser	Val	Ser	Trp	Ser	Ile	Pro	Pro	Pro	Gln	Gln	Ser		
	450					455					460						
Arg	Val	Trp	Lys	Tyr	Glu	Val	Thr	Tyr	Arg	Lys	Lys	Gly	Asp	Ser	Asn		
465					470					475					480		
Ser	Tyr	Asn	Val	Arg	Arg	Thr	Glu	Gly	Phe	Ser	Val	Thr	Leu	Asp	Asp		
				485					490					495			
Leu	Ala	Pro	Asp	Thr	Thr	Tyr	Leu	Val	Gln	Val	Gln	Ala	Leu	Thr	Gln		
			500					505					510				
Glu	Gly	Gln	Gly	Ala	Gly	Ser	Lys	Val	His	Glu	Phe	Gln	Thr	Leu	Ser		
		515					520					525					

Pro Glu Gly Ser Gly Asn Leu Ala Val Ile Gly Gly Val Ala Val Gly
 530 535 540
 Val Val Leu Leu Leu Val Leu Ala Gly Val Gly Phe Phe Ile His Arg
 545 550 555 560
 Arg Arg Lys Asn Gln Arg Ala Arg Gln Ser Pro Glu Asp Val Tyr Phe
 565 570 575
 Ser Lys Ser Glu Gln Leu Lys Pro Leu Lys Thr Tyr Val Asp Pro His
 580 585 590
 Thr Tyr Glu Asp Pro Asn Gln Ala Val Leu Lys Phe Thr Thr Glu Ile
 595 600 605
 His Pro Ser Cys Val Thr Arg Gln Lys Val Ile Gly Ala Gly Glu Phe
 610 615 620
 Gly Glu Val Tyr Lys Gly Met Leu Lys Thr Ser Ser Gly Lys Lys Glu
 625 630 635 640
 Val Pro Val Ala Ile Lys Thr Leu Lys Ala Gly Tyr Thr Glu Lys Gln
 645 650 655
 Arg Val Asp Phe Leu Gly Glu Ala Gly Ile Met Gly Gln Phe Ser His
 660 665 670
 His Asn Ile Ile Arg Leu Glu Gly Val Ile Ser Lys Tyr Lys Pro Met
 675 680 685
 Met Ile Ile Thr Glu Tyr Met Glu Asn Gly Ala Leu Asp Lys Phe Leu
 690 695 700
 Arg Glu Lys Asp Gly Glu Phe Ser Val Leu Gln Leu Val Gly Met Leu
 705 710 715 720
 Arg Gly Ile Ala Ala Gly Met Lys Tyr Leu Ala Asn Met Asn Tyr Val
 725 730 735
 His Arg Asp Leu Ala Ala Arg Asn Ile Leu Val Asn Ser Asn Leu Val
 740 745 750
 Cys Lys Val Ser Asp Phe Gly Leu Ser Arg Val Leu Glu Asp Asp Pro
 755 760 765
 Glu Ala Thr Tyr Thr Thr Ser Gly Gly Lys Ile Pro Ile Arg Trp Thr
 770 775 780
 Ala Pro Glu Ala Ile Ser Tyr Arg Lys Phe Thr Ser Ala Ser Asp Val
 785 790 795 800
 Trp Ser Phe Gly Ile Val Met Trp Glu Val Met Thr Tyr Gly Glu Arg
 805 810 815
 Pro Tyr Trp Glu Leu Ser Asn His Glu Val Met Lys Ala Ile Asn Asp
 820 825 830
 Gly Phe Arg Leu Pro Thr Pro Met Asp Cys Pro Ser Ala Ile Tyr Gln
 835 840 845
 Leu Met Met Gln Cys Trp Gln Gln Glu Arg Ala Arg Arg Pro Lys Phe

850	855	860
Ala Asp Ile Val Ser	Ile Leu Asp Lys Leu	Ile Arg Ala Pro Asp Ser
865	870	875 880
Leu Lys Thr Leu Ala	Asp Phe Asp Pro Arg	Val Ser Ile Arg Leu Pro
	885	890 895
Ser Thr Ser Gly Ser	Glu Gly Val Pro Phe	Arg Thr Val Ser Glu Trp
	900	905 910
Leu Glu Ser Ile Lys	Met Gln Gln Tyr Thr	Glu His Phe Met Ala Ala
	915	920 925
Gly Tyr Thr Ala Ile	Glu Lys Val Val Gln	Met Thr Asn Asp Asp Ile
	930	935 940
Lys Arg Ile Gly Val	Arg Leu Pro Gly His	Gln Lys Arg Ile Ala Tyr
	945	950 955 960
Ser Leu Leu Gly Leu	Lys Asp Gln Val Asn	Thr Val Gly Ile Pro Ile
	965	970 975

<210> 3
 <211> 12
 <212> PRT
 <213> Homo sapiens

<400> 3

Thr Leu Ala Asp Phe	Asp Pro Arg Val	Pro Arg Thr
1	5	10

<210> 4
 <211> 9
 <212> PRT
 <213> Homo sapiens

<400> 4

Val Leu Leu Leu Val	Leu Ala Gly Val
1	5

<210> 5
 <211> 9
 <212> PRT
 <213> Homo sapiens

<400> 5

Val Leu Ala Gly Val	Gly Phe Phe Ile
1	5

<210> 6
 <211> 9
 <212> PRT
 <213> Homo sapiens

<400> 6

Ile Met Asn Asp Met Pro Ile Tyr Met
1 5

<210> 7

<211> 9

<212> PRT

<213> Homo sapiens

<400> 7

Ser Leu Leu Gly Leu Lys Asp Gln Val
1 5

<210> 8

<211> 9

<212> PRT

<213> Homo sapiens

<400> 8

Trp Leu Val Pro Ile Gly Gln Cys Leu
1 5

<210> 9

<211> 9

<212> PRT

<213> Homo sapiens

<400> 9

Leu Leu Trp Gly Cys Ala Leu Ala Ala
1 5

<210> 10

<211> 9

<212> PRT

<213> Homo sapiens

<400> 10

Gly Leu Thr Arg Thr Ser Val Thr Val
1 5

<210> 11

<211> 9

<212> PRT

<213> Homo sapiens

<400> 11

Asn Leu Tyr Tyr Ala Glu Ser Asp Leu
1 5

<210> 12
<211> 9
<212> PRT
<213> Homo sapiens

<400> 12

Lys Leu Asn Val Glu Glu Arg Ser Val
1 5

<210> 13
<211> 9
<212> PRT
<213> Homo sapiens

<400> 13

Ile Met Gly Gln Phe Ser His His Asn
1 5

<210> 14
<211> 9
<212> PRT
<213> Homo sapiens

<400> 14

Tyr Ser Val Cys Asn Val Met Ser Gly
1 5

<210> 15
<211> 9
<212> PRT
<213> Homo sapiens

<400> 15

Met Gln Asn Ile Met Asn Asp Met Pro
1 5

<210> 16
<211> 15
<212> PRT
<213> Homo sapiens

<400> 16

Glu Ala Gly Ile Met Gly Gln Phe Ser His His Asn Ile Ile Arg
1 5 10 15

<210> 17
<211> 13
<212> PRT
<213> Homo sapiens

<400> 17

Pro Ile Tyr Met Tyr Ser Val Cys Asn Val Met Ser Gly
 1 5 10

<210> 18
 <211> 16
 <212> PRT
 <213> Homo sapiens

<400> 18

Asp Leu Met Gln Asn Ile Met Asn Asp Met Pro Ile Tyr Met Tyr Ser
 1 5 10 15

<210> 19
 <211> 3105
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Fusion construct

<400> 19
 atgaaaaaaa taatgctagt ttttattaca cttatattag ttagtctacc aattgcgcaa 60
 caaactgaag caaaggatgc atctgcattc aataaagaaa attcaatttc atccatggca 120
 ccaccagcat ctccgcctgc aagtcctaag acgccaatcg aaaagaaaca cgcggatctc 180
 gagctccagg cagcccgcgc ctgcttcgcc ctgctgtggg gctgtgcgct ggccgcggcc 240
 gcggcgggcg agggcaagga agtgggtactg ctggactttg ctgcagctgg aggggagctc 300
 ggctgggtca cacacccgta tggcaaaggg tgggacctga tgcagaacat catgaatgac 360
 atgccgatct acatgtactc cgtgtgcaac gtgatgtctg gcgaccagga caactggctc 420
 cgcaccaact ggggtgtaccg aggagaggct gagcgtatct tcattgagct caagtttact 480
 gtacgtgact gcaacagctt ccctgggtggc gccagctcct gcaaggagac tttcaacctc 540
 tactatgccg agtcggacct ggactacggc accaacttcc agaagcgcct gttcaccaag 600
 attgacacca ttgcgcccga tgagatcacc gtcagcagcg acttcgaggc acgccacgtg 660
 aagctgaacg tggaggagcg ctccgtgggg ccgctcacc gcaaaggctt ctacctggcc 720
 ttccaggata tcggtgcctg tgtggcgctg ctctccgtcc gtgtctacta caagaagtgc 780
 cccgagctgc tgcagggcct ggcccacttc cctgagacca tcgccggctc tgatgcacct 840
 tccctggcca ctgtggccgg cacctgtgtg gaccatgccg tggtgccacc ggggggtgaa 900
 gagccccgta tgcactgtgc agtggatggc gagtggctgg tgcccattgg gcagtgcctg 960
 tgccaggcag gctacgagaa ggtggaggat gcctgccagg cctgctcgcc tggatttttt 1020
 aagtttgagg catctgagag ccctgcttg gagtgccctg agcacacgct gccatccctt 1080

gaggggtgcca	cctcctgcga	gtgtgaggaa	ggcttcttcc	gggcacctca	ggacccagcg	1140
tcgatgcctt	gcacacgacc	cccctccgcc	ccacactacc	tcacagccgt	gggcatgggt	1200
gccaaggtgg	agctgcgctg	gacgccccct	caggacagcg	ggggccgcga	ggacattgtc	1260
tacagcgtea	cctgcgaaca	gtgctggccc	gagtctgggg	aatgcggggc	gtgtgaggcc	1320
agtgtgcgct	actcggagcc	tcctcacgga	ctgaccgcga	ccagtgtgac	agtgagcgac	1380
ctggagcccc	acatgaacta	caccttcacc	gtggaggccc	gcaatggcgt	ctcaggcctg	1440
gtaaccagcc	gcagcttccg	tactgccagt	gtcagcatca	accagacaga	gcccccaag	1500
gtgaggctgg	agggccgcag	caccacctcg	cttagcgtct	cctggagcat	ccccccgccg	1560
cagcagagcc	gagtgtggaa	gtacgaggtc	acttaccgca	agaagggaga	ctccaacagc	1620
tacaatgtgc	gccgcaccga	gggtttctcc	gtgaccctgg	acgacctggc	cccagacacc	1680
acctacctgg	tccaggtgca	ggcactgacg	caggagggcc	agggggccgg	cagcaggggtg	1740
cacgaattcc	agacgctgtc	cccgagggga	tctggcaact	tggcggtgat	tggcggcgtg	1800
gctgtcggtg	tggtcctgct	tctggtgctg	gcaggagttg	gcttctttat	ccaccgcagg	1860
aggaagaacc	agcgtgcccc	ccagtccccg	gaggacgttt	acttctccaa	gtcagaacaa	1920
ctgaagcccc	tgaagacata	cgtggacccc	cacacatatg	aggaccccaa	ccaggctgtg	1980
ttgaagttca	ctaccgagat	ccatccatcc	tgtgtcactc	ggcagaaggt	gatcggagca	2040
ggagagtttg	gggaggtgta	caagggcatg	ctgaagacat	cctcggggaa	gaaggaggtg	2100
ccggtggcca	tcaagacgct	gaaagccggc	tacacagaga	agcagcgagt	ggacttcctc	2160
ggcgaggccg	gcatcatggg	ccagttcagc	caccacaaca	tcacccgcct	agagggcgtc	2220
atctccaaat	acaagcccat	gatgatcatc	actgagtaca	tggagaatgg	ggccctggac	2280
aagttccttc	gggagaagga	tggcgagttc	agcgtgctgc	agctggtggg	catgctgcgg	2340
ggcatcgcag	ctggcatgaa	gtacctggcc	aacatgaact	atgtgcaccg	tgacctggct	2400
gcccgcgaaca	tcctcgtcaa	cagcaacctg	gtctgcaagg	tgtctgactt	tggcctgtcc	2460
cgcgtgctgg	aggacgaccc	cgaggccacc	tacaccacca	gtggcggcaa	gatccccatc	2520
cgttggaacc	ccccggaggc	catttcctac	cggaaagttca	cctctgccag	cgacgtgtgg	2580
agctttggca	ttgtcatgtg	ggaggtgatg	acctatggcg	agcggcccta	ctgggagttg	2640
tccaaccacg	aggtgatgaa	agccatcaat	gatggcttcc	ggctccccac	acccatggac	2700
tgccccctcc	ccatctacca	gctcatgatg	cagtgtggc	agcaggagcg	tgcccgcgc	2760
cccaagttcg	ctgacatcgt	cagcatcctg	gacaagctca	ttcgtgcccc	tgactccctc	2820
aagaccctgg	ctgactttga	ccccgcgtg	tctatccggc	tccccagcac	gagcggctcg	2880
gaggggggtgc	ccttccgcac	ggtgtccgag	tggctggagt	ccatcaagat	gcagcagtat	2940

acggagcact tcattggcggc cggctacact gccatcgaga aggtggtgca gatgaccaac 3000
gacgacatca agaggattgg ggtgcggctg cccggccacc agaagcgcat cgcctacagc 3060
ctgctgggac tcaaggacca ggtgaacact gtggggatcc ccatac 3105

<210> 20
<211> 1035
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Predicted fusion protein

<400> 20

Met	Lys	Lys	Ile	Met	Leu	Val	Phe	Ile	Thr	Leu	Ile	Leu	Val	Ser	Leu	1	5	10	15
Pro	Ile	Ala	Gln	Gln	Thr	Glu	Ala	Lys	Asp	Ala	Ser	Ala	Phe	Asn	Lys	20	25	30	
Glu	Asn	Ser	Ile	Ser	Ser	Met	Ala	Pro	Pro	Ala	Ser	Pro	Pro	Ala	Ser	35	40	45	
Pro	Lys	Thr	Pro	Ile	Glu	Lys	Lys	His	Ala	Asp	Leu	Glu	Leu	Gln	Ala	50	55	60	
Ala	Arg	Ala	Cys	Phe	Ala	Leu	Leu	Trp	Gly	Cys	Ala	Leu	Ala	Ala	Ala	65	70	75	80
Ala	Ala	Ala	Gln	Gly	Lys	Glu	Val	Val	Leu	Leu	Asp	Phe	Ala	Ala	Ala	85	90	95	
Gly	Gly	Glu	Leu	Gly	Trp	Leu	Thr	His	Pro	Tyr	Gly	Lys	Gly	Trp	Asp	100	105	110	
Leu	Met	Gln	Asn	Ile	Met	Asn	Asp	Met	Pro	Ile	Tyr	Met	Tyr	Ser	Val	115	120	125	
Cys	Asn	Val	Met	Ser	Gly	Asp	Gln	Asp	Asn	Trp	Leu	Arg	Thr	Asn	Trp	130	135	140	
Val	Tyr	Arg	Gly	Glu	Ala	Glu	Arg	Ile	Phe	Ile	Glu	Leu	Lys	Phe	Thr	145	150	155	160
Val	Arg	Asp	Cys	Asn	Ser	Phe	Pro	Gly	Gly	Ala	Ser	Ser	Cys	Lys	Glu	165	170	175	
Thr	Phe	Asn	Leu	Tyr	Tyr	Ala	Glu	Ser	Asp	Leu	Asp	Tyr	Gly	Thr	Asn	180	185	190	
Phe	Gln	Lys	Arg	Leu	Phe	Thr	Lys	Ile	Asp	Thr	Ile	Ala	Pro	Asp	Glu	195	200	205	
Ile	Thr	Val	Ser	Ser	Asp	Phe	Glu	Ala	Arg	His	Val	Lys	Leu	Asn	Val	210	215	220	
Glu	Glu	Arg	Ser	Val	Gly	Pro	Leu	Thr	Arg	Lys	Gly	Phe	Tyr	Leu	Ala				

Thr Tyr Leu Val Gln Val Gln Ala Leu Thr Gln Glu Gly Gln Gly Ala
 565 570 575
 Gly Ser Arg Val His Glu Phe Gln Thr Leu Ser Pro Glu Gly Ser Gly
 580 585 590
 Asn Leu Ala Val Ile Gly Gly Val Ala Val Gly Val Val Leu Leu Leu
 595 600 605
 Val Leu Ala Gly Val Gly Phe Phe Ile His Arg Arg Arg Lys Asn Gln
 610 615 620
 Arg Ala Arg Gln Ser Pro Glu Asp Val Tyr Phe Ser Lys Ser Glu Gln
 625 630 635 640
 Leu Lys Pro Leu Lys Thr Tyr Val Asp Pro His Thr Tyr Glu Asp Pro
 645 650 655
 Asn Gln Ala Val Leu Lys Phe Thr Thr Glu Ile His Pro Ser Cys Val
 660 665 670
 Thr Arg Gln Lys Val Ile Gly Ala Gly Glu Phe Gly Glu Val Tyr Lys
 675 680 685
 Gly Met Leu Lys Thr Ser Ser Gly Lys Lys Glu Val Pro Val Ala Ile
 690 695 700
 Lys Thr Leu Lys Ala Gly Tyr Thr Glu Lys Gln Arg Val Asp Phe Leu
 705 710 715 720
 Gly Glu Ala Gly Ile Met Gly Gln Phe Ser His His Asn Ile Ile Arg
 725 730 735
 Leu Glu Gly Val Ile Ser Lys Tyr Lys Pro Met Met Ile Ile Thr Glu
 740 745 750
 Tyr Met Glu Asn Gly Ala Leu Asp Lys Phe Leu Arg Glu Lys Asp Gly
 755 760 765
 Glu Phe Ser Val Leu Gln Leu Val Gly Met Leu Arg Gly Ile Ala Ala
 770 775 780
 Gly Met Lys Tyr Leu Ala Asn Met Asn Tyr Val His Arg Asp Leu Ala
 785 790 795 800
 Ala Arg Asn Ile Leu Val Asn Ser Asn Leu Val Cys Lys Val Ser Asp
 805 810 815
 Phe Gly Leu Ser Arg Val Leu Glu Asp Asp Pro Glu Ala Thr Tyr Thr
 820 825 830
 Thr Ser Gly Gly Lys Ile Pro Ile Arg Trp Thr Ala Pro Glu Ala Ile
 835 840 845
 Ser Tyr Arg Lys Phe Thr Ser Ala Ser Asp Val Trp Ser Phe Gly Ile
 850 855 860
 Val Met Trp Glu Val Met Thr Tyr Gly Glu Arg Pro Tyr Trp Glu Leu
 865 870 875 880

Ser Asn His Glu Val Met Lys Ala Ile Asn Asp Gly Phe Arg Leu Pro
 885 890 895
 Thr Pro Met Asp Cys Pro Ser Ala Ile Tyr Gln Leu Met Met Gln Cys
 900 905 910
 Trp Gln Gln Glu Arg Ala Arg Arg Pro Lys Phe Ala Asp Ile Val Ser
 915 920 925
 Ile Leu Asp Lys Leu Ile Arg Ala Pro Asp Ser Leu Lys Thr Leu Ala
 930 935 940
 Asp Phe Asp Pro Arg Val Ser Ile Arg Leu Pro Ser Thr Ser Gly Ser
 945 950 955 960
 Glu Gly Val Pro Phe Arg Thr Val Ser Glu Trp Leu Glu Ser Ile Lys
 965 970 975
 Met Gln Gln Tyr Thr Glu His Phe Met Ala Ala Gly Tyr Thr Ala Ile
 980 985 990
 Glu Lys Val Val Gln Met Thr Asn Asp Asp Ile Lys Arg Ile Gly Val
 995 1000 1005
 Arg Leu Pro Gly His Gln Lys Arg Ile Ala Tyr Ser Leu Leu Gly
 1010 1015 1020
 Leu Lys Asp Gln Val Asn Thr Val Gly Ile Pro Ile
 1025 1030 1035

<210> 21
 <211> 1506
 <212> DNA
 <213> Homo sapiens

<400> 21
 cagggcaagg aagtggact gctggacttt gctgcagctg gaggggagct cggctggctc 60
 acacacccgt atggcaaagg gtgggacctg atgcagaaca tcatgaatga catgccgac 120
 tacatgtact ccgtgtgcaa cgtgatgtct ggcgaccagg acaactggct ccgcaccaac 180
 tgggtgtacc gaggagaggc tgagcgtatc ttcattgagc tcaagtttac tgtacgtgac 240
 tgcaacagct tccctggtgg cgccagctcc tgcaaggaga ctttcaacct ctactatgcc 300
 gagtgggacc tggactacgg caccaacttc cagaagcgcc tgttcaccaa gattgacacc 360
 attgcgcccg atgagatcac cgtcagcagc gacttcgagg cacgccacgt gaagctgaac 420
 gtggaggagc gctccgtggg gccgctcacc cgcaaaggct tctacctggc cttccaggat 480
 atcgggtgcct gtgtggcgct gctctccgtc cgtgtctact acaagaagtg ccccgagctg 540
 ctgcagggcc tggcccactt ccctgagacc atcgccggct ctgatgcacc ttccctggcc 600
 actgtggccg gcacctgtgt ggaccatgcc gtggtgccac cgggggggtga agagccccgt 660
 atgcactgtg cagtggatgg cgagtggctg gtgcccattg ggcagtgcct gtgccaggca 720

ggctacgaga aggtggagga tgcctgccag gcctgctcgc ctggattttt taagtttgag	780
gcatctgaga gcccctgctt ggagtgcctt gagcacacgc tgccatcccc tgagggtgcc	840
acctcctgcg agtgtaggga aggttcttctc cgggcacctc aggacccagc gtcgatgcct	900
tgcacacgac ccccctccgc cccacactac ctacagccg tgggcatggg tgccaagggtg	960
gagctgcgct ggacgcccc tcaggacagc gggggccgcg aggacattgt ctacagcgtc	1020
acctgcgaac agtgctggcc cgagtctggg gaatgcgggc cgtgtgaggc cagtgtgcgc	1080
tactcggagc ctccctcacg actgaccgc accagtgtga cagtgagcga cctggagccc	1140
cacatgaact acaccttcac cgtggaggcc cgcaatggcg tctcaggcct ggtaaccagc	1200
cgcagcttcc gtactgccag tgtcagcatc aaccagacag agcccccaa ggtgaggctg	1260
gagggccgca gcaccacctc gcttagcgtc tcttgagca tcccccgcc gcagcagagc	1320
cgagtgtgga agtacgaggt cacttaccgc aagaaggag actccaacag ctacaatgtg	1380
cgccgcaccg agggtttctc cgtgaccctg gacgacctg cccagacac cacctacctg	1440
gtccagggtgc aggactgac gcaggagggc cagggggccg gcagcagggt gcacgaattc	1500
cagacg	1506

<210> 22
 <211> 1506
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Human sequence optimized for codon usage in *Listeria*

<400> 22	
caaggtaaag aagttgtttt attagatttt gcagcagcag gtggtgaatt aggttggtta	60
acacatccat atggtaaagg ttgggattta atgcaaaata ttatgaatga tatgccaatt	120
tatatgtata gtgtttgtaa tgttatgagt ggtgatcaag ataattggtt acgtacaaat	180
tgggtttatc gtggtgaagc agaacgtatt tttattgaat taaaatttac agttcgtgat	240
tgtaatagtt ttccagggtg tgcaagtagt tgtaagaaa catttaattt atattatgca	300
gaaagtgatt tagattatgg tacaaatttt caaaaacggt tattttacaaa aattgataca	360
attgcaccag atgaaattac agttagtagt gattttgaag cacgtcatgt taaattaaat	420
gttgaagaac gtagtgttgg tccattaaca cgtaaagggt tttatttagc atttcaagat	480
attggtgcat gtgttgcatt attaagtgtt cgtgtttatt ataaaaaatg tccagaatta	540
ttacaagggt tagcacattt tccagaaaca attgcaggta gtgatgcacc aagtttagca	600
acagttgcag gtacatgtgt tgatcatgca gttgttccac caggtggtga agaaccacgt	660

atgcattgtg cagttgatgg tgaatggta gttccaattg gtcaatgttt atgtcaagca 720
 ggttatgaaa aagttgaaga tgcattgtcaa gcatgtagtc cagggtttttt taaatttgaa 780
 gcaagtgaaa gtccatgtttt agaattgtcca gaacatacat taccaagtcc agaagggtgca 840
 acaagttgtg aatgtgaaga aggtttttttt cgtgcaccac aagatccagc aagtatgcca 900
 tgtacacgtc caccaagtgc accacattat ttaacagcag ttggtatggg tgcaaaagtt 960
 gaattacgtt ggacaccacc acaagatagt ggtggtcgtg aagatattgt ttatagtgtt 1020
 acatgtgaac aatgttggcc agaaagtggg gaatgtggtc catgtgaagc aagtgttcgt 1080
 tatagtgaac caccacatgg tttaacacgt acaagtgtta cagttagtga tttagaacca 1140
 catatgaatt atacattttac agttgaagca cgtaatgggtg ttagtggttt agttacaagt 1200
 cgtagttttc gtacagcaag tgtagtatt aatcaaacag aaccaccaa agttcgttta 1260
 gaaggtcgta gtacaacaag tttaagtgtt agttggagta ttccaccacc acaacaaagt 1320
 cgtgttttga aatatgaagt tacatatcgt aaaaaagggtg atagtaatag ttataatgtt 1380
 cgtcgtacag aagggttttag tgttacatta gatgatttag caccagatac aacatattta 1440
 gttcaagttc aagcattaac acaagaaggt caagggtgcag gtagtcgtgt tcatgaattt 1500
 caaaca 1506

<210> 23
 <211> 502
 <212> PRT
 <213> Homo sapeins

<400> 23

Gln Gly Lys Glu Val Val Leu Leu Asp Phe Ala Ala Ala Gly Gly Glu
 1 5 10 15
 Leu Gly Trp Leu Thr His Pro Tyr Gly Lys Gly Trp Asp Leu Met Gln
 20 25 30
 Asn Ile Met Asn Asp Met Pro Ile Tyr Met Tyr Ser Val Cys Asn Val
 35 40 45
 Met Ser Gly Asp Gln Asp Asn Trp Leu Arg Thr Asn Trp Val Tyr Arg
 50 55 60
 Gly Glu Ala Glu Arg Ile Phe Ile Glu Leu Lys Phe Thr Val Arg Asp
 65 70 75 80
 Cys Asn Ser Phe Pro Gly Gly Ala Ser Ser Cys Lys Glu Thr Phe Asn
 85 90 95
 Leu Tyr Tyr Ala Glu Ser Asp Leu Asp Tyr Gly Thr Asn Phe Gln Lys
 100 105 110
 Arg Leu Phe Thr Lys Ile Asp Thr Ile Ala Pro Asp Glu Ile Thr Val
 115 120 125

Ser	Ser	Asp	Phe	Glu	Ala	Arg	His	Val	Lys	Leu	Asn	Val	Glu	Glu	Arg	
130						135					140					
Ser	Val	Gly	Pro	Leu	Thr	Arg	Lys	Gly	Phe	Tyr	Leu	Ala	Phe	Gln	Asp	
145					150					155					160	
Ile	Gly	Ala	Cys	Val	Ala	Leu	Leu	Ser	Val	Arg	Val	Tyr	Tyr	Lys	Lys	
				165					170					175		
Cys	Pro	Glu	Leu	Leu	Gln	Gly	Leu	Ala	His	Phe	Pro	Glu	Thr	Ile	Ala	
			180					185					190			
Gly	Ser	Asp	Ala	Pro	Ser	Leu	Ala	Thr	Val	Ala	Gly	Thr	Cys	Val	Asp	
		195					200					205				
His	Ala	Val	Val	Pro	Pro	Gly	Gly	Glu	Glu	Pro	Arg	Met	His	Cys	Ala	
						215					220					
Val	Asp	Gly	Glu	Trp	Leu	Val	Pro	Ile	Gly	Gln	Cys	Leu	Cys	Gln	Ala	
225					230					235					240	
Gly	Tyr	Glu	Lys	Val	Glu	Asp	Ala	Cys	Gln	Ala	Cys	Ser	Pro	Gly	Phe	
				245					250					255		
Phe	Lys	Phe	Glu	Ala	Ser	Glu	Ser	Pro	Cys	Leu	Glu	Cys	Pro	Glu	His	
			260					265					270			
Thr	Leu	Pro	Ser	Pro	Glu	Gly	Ala	Thr	Ser	Cys	Glu	Cys	Glu	Glu	Gly	
		275					280						285			
Phe	Phe	Arg	Ala	Pro	Gln	Asp	Pro	Ala	Ser	Met	Pro	Cys	Thr	Arg	Pro	
		290				295					300					
Pro	Ser	Ala	Pro	His	Tyr	Leu	Thr	Ala	Val	Gly	Met	Gly	Ala	Lys	Val	
305					310					315					320	
Glu	Leu	Arg	Trp	Thr	Pro	Pro	Gln	Asp	Ser	Gly	Gly	Arg	Glu	Asp	Ile	
				325					330					335		
Val	Tyr	Ser	Val	Thr	Cys	Glu	Gln	Cys	Trp	Pro	Glu	Ser	Gly	Glu	Cys	
			340					345					350			
Gly	Pro	Cys	Glu	Ala	Ser	Val	Arg	Tyr	Ser	Glu	Pro	Pro	His	Gly	Leu	
		355					360					365				
Thr	Arg	Thr	Ser	Val	Thr	Val	Ser	Asp	Leu	Glu	Pro	His	Met	Asn	Tyr	
		370				375					380					
Thr	Phe	Thr	Val	Glu	Ala	Arg	Asn	Gly	Val	Ser	Gly	Leu	Val	Thr	Ser	
385					390					395					400	
Arg	Ser	Phe	Arg	Thr	Ala	Ser	Val	Ser	Ile	Asn	Gln	Thr	Glu	Pro	Pro	
				405					410					415		
Lys	Val	Arg	Leu	Glu	Gly	Arg	Ser	Thr	Thr	Ser	Leu	Ser	Val	Ser	Trp	
			420					425					430			
Ser	Ile	Pro	Pro	Pro	Gln	Gln	Ser	Arg	Val	Trp	Lys	Tyr	Glu	Val	Thr	
		435					440					445				

Tyr Arg Lys Lys Gly Asp Ser Asn Ser Tyr Asn Val Arg Arg Thr Glu
 450 455 460
 Gly Phe Ser Val Thr Leu Asp Asp Leu Ala Pro Asp Thr Thr Tyr Leu
 465 470 475 480
 Val Gln Val Gln Ala Leu Thr Gln Glu Gly Gln Gly Ala Gly Ser Arg
 485 490 495
 Val His Glu Phe Gln Thr
 500

<210> 24
 <211> 1689
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Fusion protein construct

<400> 24
 atgaaaaaaa taatgctagt ttttattaca cttatattag ttagtctacc aattgcgcaa 60
 caaactgaag caaaggatgc atctgcattc aataaagaaa attcaatttc atccatggca 120
 ccaccagcat ctccgcctgc aagtcctaag acgccaatcg aaaagaaaca cgcggatctc 180
 gagcagggca aggaagtggc actgctggac tttgctgcag ctggagggga gctcggctgg 240
 ctcacacacc cgtatggcaa aggggtgggac ctgatgcaga acatcatgaa tgacatgccg 300
 atctacatgt actccgtgtg caacgtgatg tctggcgacc aggacaactg gctccgcacc 360
 aactgggtgt accgaggaga ggctgagcgt atcttcattg agctcaagtt tactgtacgt 420
 gactgcaaca gcttccctgg tggcgccagc tcctgcaagg agactttcaa cctctactat 480
 gccgagtcgg acctggacta cggcaccaac ttccagaagc gcctgttcac caagattgac 540
 accattgcgc ccgatgagat caccgtcagc agcgacttcg aggcacgcca cgtgaagctg 600
 aacgtggagg agcgctccgt ggggccgctc acccgcaaag gcttctacct ggccttcag 660
 gatatcgggtg cctgtgtggc gctgctctcc gtccgtgtct actacaagaa gtgccccgag 720
 ctgctgcagg gcctggccca cttccctgag accatcgccg gctctgatgc accttccctg 780
 gccactgtgg ccggcacctg tgtggacat gccgtggtgc caccgggggg tgaagagccc 840
 cgtatgcact gtgcagtgga tggcgagtgg ctggtgccca ttgggcagtg cctgtgccag 900
 gcaggctacg agaaggtgga ggatgcctgc caggcctgct cgcttgatt ttttaagttt 960
 gaggcattctg agagcccctg cttggagtgc cctgagcaca cgctgccatc ccctgagggg 1020
 gccacctcct gcgagtgtga ggaaggcttc ttccgggcac ctccaggacc agcgtcgatg 1080
 ccttgcacac gacccccctc cgccccacac tacctcacag ccgtgggcat gggtgccaag 1140
 gtggagctgc gctggacgcc ccctcaggac agcggggggc gcgaggacat tgtctacagc 1200

gtcacctgcg aacagtgctg gcccgagtct ggggaatgcg ggccgtgtga ggccagtgtg 1260
cgctactcgg agcctcctca cggactgacc cgcaccagtg tgacagtgag cgacctggag 1320
ccccacatga actacacctt caccgtggag gcccgcaatg gcgtctcagg cctggtaacc 1380
agccgcagct tccgtactgc cagtgtcagc atcaaccaga cagagccccc caaggtgagg 1440
ctggaggggcc gcagcaccac ctcgcttagc gtctcctgga gcatcccccc gccgcagcag 1500
agccgagtgt ggaagtacga ggtcacttac cgcaagaagg gagactccaa cagctacaat 1560
gtgcgccgca ccgaggggtt ctccgtgacc ctggacgacc tggccccaga caccacctac 1620
ctggtccagg tgcaggcact gacgcaggag ggccaggggg ccggcagcag ggtgcacgaa 1680
ttccagacg 1689

<210> 25

<211> 563

<212> PRT

<213> Artificial Sequence

<220> .

<223> Description of Artificial Sequence: Predicted fusion protein

<400> . 25

Met	Lys	Lys	Ile	Met	Leu	Val	Phe	Ile	Thr	Leu	Ile	Leu	Val	Ser	Leu	1	5	10	15
Pro	Ile	Ala	Gln	Gln	Thr	Glu	Ala	Lys	Asp	Ala	Ser	Ala	Phe	Asn	Lys	20	25	30	
Glu	Asn	Ser	Ile	Ser	Ser	Met	Ala	Pro	Pro	Ala	Ser	Pro	Pro	Ala	Ser	35	40	45	
Pro	Lys	Thr	Pro	Ile	Glu	Lys	Lys	His	Ala	Asp	Leu	Glu	Gln	Gly	Lys	50	55	60	
Glu	Val	Val	Leu	Leu	Asp	Phe	Ala	Ala	Ala	Gly	Gly	Glu	Leu	Gly	Trp	65	70	75	80
Leu	Thr	His	Pro	Tyr	Gly	Lys	Gly	Trp	Asp	Leu	Met	Gln	Asn	Ile	Met	85	90	95	
Asn	Asp	Met	Pro	Ile	Tyr	Met	Tyr	Ser	Val	Cys	Asn	Val	Met	Ser	Gly	100	105	110	
Asp	Gln	Asp	Asn	Trp	Leu	Arg	Thr	Asn	Trp	Val	Tyr	Arg	Gly	Glu	Ala	115	120	125	
Glu	Arg	Ile	Phe	Ile	Glu	Leu	Lys	Phe	Thr	Val	Arg	Asp	Cys	Asn	Ser	130	135	140	
Phe	Pro	Gly	Gly	Ala	Ser	Ser	Cys	Lys	Glu	Thr	Phe	Asn	Leu	Tyr	Tyr	145	150	155	160
Ala	Glu	Ser	Asp	Leu	Asp	Tyr	Gly	Thr	Asn	Phe	Gln	Lys	Arg	Leu	Phe				

165					170					175					
Thr	Lys	Ile	Asp	Thr	Ile	Ala	Pro	Asp	Glu	Ile	Thr	Val	Ser	Ser	Asp
			180					185					190		
Phe	Glu	Ala	Arg	His	Val	Lys	Leu	Asn	Val	Glu	Glu	Arg	Ser	Val	Gly
		195					200					205			
Pro	Leu	Thr	Arg	Lys	Gly	Phe	Tyr	Leu	Ala	Phe	Gln	Asp	Ile	Gly	Ala
	210					215					220				
Cys	Val	Ala	Leu	Leu	Ser	Val	Arg	Val	Tyr	Tyr	Lys	Lys	Cys	Pro	Glu
225					230					235					240
Leu	Leu	Gln	Gly	Leu	Ala	His	Phe	Pro	Glu	Thr	Ile	Ala	Gly	Ser	Asp
				245					250					255	
Ala	Pro	Ser	Leu	Ala	Thr	Val	Ala	Gly	Thr	Cys	Val	Asp	His	Ala	Val
			260					265					270		
Val	Pro	Pro	Gly	Gly	Glu	Glu	Pro	Arg	Met	His	Cys	Ala	Val	Asp	Gly
		275					280					285			
Glu	Trp	Leu	Val	Pro	Ile	Gly	Gln	Cys	Leu	Cys	Gln	Ala	Gly	Tyr	Glu
	290					295					300				
Lys	Val	Glu	Asp	Ala	Cys	Gln	Ala	Cys	Ser	Pro	Gly	Phe	Phe	Lys	Phe
305					310					315					320
Glu	Ala	Ser	Glu	Ser	Pro	Cys	Leu	Glu	Cys	Pro	Glu	His	Thr	Leu	Pro
				325					330					335	
Ser	Pro	Glu	Gly	Ala	Thr	Ser	Cys	Glu	Cys	Glu	Glu	Gly	Phe	Phe	Arg
			340					345					350		
Ala	Pro	Gln	Asp	Pro	Ala	Ser	Met	Pro	Cys	Thr	Arg	Pro	Pro	Ser	Ala
		355					360					365			
Pro	His	Tyr	Leu	Thr	Ala	Val	Gly	Met	Gly	Ala	Lys	Val	Glu	Leu	Arg
	370					375					380				
Trp	Thr	Pro	Pro	Gln	Asp	Ser	Gly	Gly	Arg	Glu	Asp	Ile	Val	Tyr	Ser
385					390					395					400
Val	Thr	Cys	Glu	Gln	Cys	Trp	Pro	Glu	Ser	Gly	Glu	Cys	Gly	Pro	Cys
				405					410					415	
Glu	Ala	Ser	Val	Arg	Tyr	Ser	Glu	Pro	Pro	His	Gly	Leu	Thr	Arg	Thr
			420					425					430		
Ser	Val	Thr	Val	Ser	Asp	Leu	Glu	Pro	His	Met	Asn	Tyr	Thr	Phe	Thr
		435				440					445				
Val	Glu	Ala	Arg	Asn	Gly	Val	Ser	Gly	Leu	Val	Thr	Ser	Arg	Ser	Phe
	450					455					460				
Arg	Thr	Ala	Ser	Val	Ser	Ile	Asn	Gln	Thr	Glu	Pro	Pro	Lys	Val	Arg
465					470					475					480
Leu	Glu	Gly	Arg	Ser	Thr	Thr	Ser	Leu	Ser	Val	Ser	Trp	Ser	Ile	Pro
				485					490					495	

Pro Pro Gln Gln Ser Arg Val Trp Lys Tyr Glu Val Thr Tyr Arg Lys
500 505 510

Lys Gly Asp Ser Asn Ser Tyr Asn Val Arg Arg Thr Glu Gly Phe Ser
515 520 525

Val Thr Leu Asp Asp Leu Ala Pro Asp Thr Thr Tyr Leu Val Gln Val
530 535 540

Gln Ala Leu Thr Gln Glu Gly Gln Gly Ala Gly Ser Arg Val His Glu
545 550 555 560

Phe Gln Thr

<210> 26
<211> 1989
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Fusion protein construct

<400> 26
ggtacctcct ttgattagta tttcctatc ttaaagttac ttttatgtgg aggcattaac 60
atttggttaat gacgtcaaaa ggatagcaag actagaataa agctataaag caagcatata 120
atattgcggt tcatctttag aagcgaattt cgccaatatt ataattatca aaagagaggg 180
gtggcacaacg gtatttggca ttattaggtt aaaaaatgta gaaggagagt gaaacccatg 240
aaaaaaataa tgctagtgtt tattacactt atattagtta gtctaccaat tgcgcaacaa 300
actgaagcaa aggatgcatc tgcattcaat aaagaaaatt caatttcac ccatggcacca 360
ccagcatctc cgccctgcaag tcctaagacg ccaatcgaaa agaaacacgc ggatggatcc 420
gattataaag atgatgatga taaacaaggt aaagaagttg ttttattaga ttttcagca 480
gcaggtggtg aattaggttg gttaacacat ccatatggta aaggttgga tttaatgcaa 540
aatattatga atgatatgcc aatttatatg tatagtgtt gtaatgttat gagtggatgat 600
caagataaatt gggtacgtac aaattgggtt tatcgtggtg aagcagaacg tttttttatt 660
gaattaaaat ttacagttcg tgattgtaat agttttccag gtggtgcaag tagttgtaaa 720
gaaacattta atttatatta tgcagaaagt gatttagatt atggtacaaa ttttcaaaaa 780
cgtttattta caaaaattga tacaattgca ccagatgaaa ttacagttag tagtgatttt 840
gaagcacgtc atgttaaatt aaatgttgaa gaacgtagtg ttggtccatt aacacgtaaa 900
ggtttttatt tagcatttca agatattggg gcatgtgttg cattattaag tgttcgtgtt 960
tattataaaa aatgtccaga attattacaa ggttttagcac attttccaga aacaattgca 1020
ggtagtgatg caccaagttt agcaacagtt gcaggtacat gtgttgatca tgcagttgtt 1080


```

ccaccagggtg gtgaagaacc acgtatgcat tgtgcagttg atggtgaatg gttagttcca 1140
attggtcaat gtttatgtca agcaggttat gaaaaagttg aagatgcatg tcaagcatgt 1200
agtccagggtt tttttaaatt tgaagcaagt gaaagtccat gtttagaatg tccagaacat 1260
acattaccaa gtccagaagg tgcaacaagt tgtgaatgtg aagaaggttt ttttcgtgca 1320
ccacaagatc cagcaagtat gccatgtaca cgtccaccaa gtgcaccaca ttatttaaca 1380
gcagttggta tgggtgcaaa agttgaatta cgttggacac caccacaaga tagtgggtgg 1440
cgtgaagata ttgtttatag tgttacatgt gaacaatgtt ggccagaaag tgggtgaatgt 1500
gggccatgtg aagcaagtgt tcgttatagt gaaccaccac atgggtttaac acgtacaagt 1560
gttacagtta gtgatttaga accacatatg aattatacat ttacagttga agcacgtaat 1620
gggtgttagtg gtttagttac aagtcgtagt tttcgtacag caagtgttag tattaatcaa 1680
acagaaccac caaaagttcg tttagaaggt cgtagtacaa caagtttaag tgtagttgg 1740
agtattccac caccacaaca aagtcgtgtt tggaaatatg aagttacata tcgtaaaaaa 1800
ggtgatagta atagttataa tgttcgtcgt acagaagggt ttagtggttac attagatgat 1860
ttagcaccag atacaacata tttagttcaa gttcaagcat taacacaaga aggtcaagg 1920
gcaggtagtc gtgttcatga atttcaaaca gaacaaaaat taattagtga agaagattta 1980
tgagagctc 1989

```

```

<210> 27
<211> 581
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> Description of Artificial Sequence: Predicted fusion protein

```

```

<400> 27

```

```

Met Lys Lys Ile Met Leu Val Phe Ile Thr Leu Ile Leu Val Ser Leu
1           5           10          15
Pro Ile Ala Gln Gln Thr Glu Ala Lys Asp Ala Ser Ala Phe Asn Lys
          20          25          30
Glu Asn Ser Ile Ser Ser Met Ala Pro Pro Ala Ser Pro Pro Ala Ser
          35          40          45
Pro Lys Thr Pro Ile Glu Lys Lys His Ala Asp Gly Ser Asp Tyr Lys
          50          55          60
Asp Asp Asp Asp Lys Gln Gly Lys Glu Val Val Leu Leu Asp Phe Ala
65          70          75          80
Ala Ala Gly Gly Glu Leu Gly Trp Leu Thr His Pro Tyr Gly Lys Gly
          85          90          95

```

Trp	Asp	Leu	Met	Gln	Asn	Ile	Met	Asn	Asp	Met	Pro	Ile	Tyr	Met	Tyr		
			100					105					110				
Ser	Val	Cys	Asn	Val	Met	Ser	Gly	Asp	Gln	Asp	Asn	Trp	Leu	Arg	Thr		
		115					120					125					
Asn	Trp	Val	Tyr	Arg	Gly	Glu	Ala	Glu	Arg	Ile	Phe	Ile	Glu	Leu	Lys		
	130					135					140						
Phe	Thr	Val	Arg	Asp	Cys	Asn	Ser	Phe	Pro	Gly	Gly	Ala	Ser	Ser	Cys		
145					150					155					160		
Lys	Glu	Thr	Phe	Asn	Leu	Tyr	Tyr	Ala	Glu	Ser	Asp	Leu	Asp	Tyr	Gly		
				165					170					175			
Thr	Asn	Phe	Gln	Lys	Arg	Leu	Phe	Thr	Lys	Ile	Asp	Thr	Ile	Ala	Pro		
			180					185					190				
Asp	Glu	Ile	Thr	Val	Ser	Ser	Asp	Phe	Glu	Ala	Arg	His	Val	Lys	Leu		
	195						200					205					
Asn	Val	Glu	Glu	Arg	Ser	Val	Gly	Pro	Leu	Thr	Arg	Lys	Gly	Phe	Tyr		
	210					215					220						
Leu	Ala	Phe	Gln	Asp	Ile	Gly	Ala	Cys	Val	Ala	Leu	Leu	Ser	Val	Arg		
225					230					235					240		
Val	Tyr	Tyr	Lys	Lys	Cys	Pro	Glu	Leu	Leu	Gln	Gly	Leu	Ala	His	Phe		
				245					250					255			
Pro	Glu	Thr	Ile	Ala	Gly	Ser	Asp	Ala	Pro	Ser	Leu	Ala	Thr	Val	Ala		
			260					265					270				
Gly	Thr	Cys	Val	Asp	His	Ala	Val	Val	Pro	Pro	Gly	Gly	Glu	Glu	Pro		
	275						280					285					
Arg	Met	His	Cys	Ala	Val	Asp	Gly	Glu	Trp	Leu	Val	Pro	Ile	Gly	Gln		
	290					295					300						
Cys	Leu	Cys	Gln	Ala	Gly	Tyr	Glu	Lys	Val	Glu	Asp	Ala	Cys	Gln	Ala		
305					310					315					320		
Cys	Ser	Pro	Gly	Phe	Phe	Lys	Phe	Glu	Ala	Ser	Glu	Ser	Pro	Cys	Leu		
				325					330					335			
Glu	Cys	Pro	Glu	His	Thr	Leu	Pro	Ser	Pro	Glu	Gly	Ala	Thr	Ser	Cys		
			340					345					350				
Glu	Cys	Glu	Glu	Gly	Phe	Phe	Arg	Ala	Pro	Gln	Asp	Pro	Ala	Ser	Met		
		355					360					365					
Pro	Cys	Thr	Arg	Pro	Pro	Ser	Ala	Pro	His	Tyr	Leu	Thr	Ala	Val	Gly		
		370				375					380						
Met	Gly	Ala	Lys	Val	Glu	Leu	Arg	Trp	Thr	Pro	Pro	Gln	Asp	Ser	Gly		
385					390					395					400		
Gly	Arg	Glu	Asp	Ile	Val	Tyr	Ser	Val	Thr	Cys	Glu	Gln	Cys	Trp	Pro		
				405					410					415			

Glu Ser Gly Glu Cys Gly Pro Cys Glu Ala Ser Val Arg Tyr Ser Glu
 420 425 430
 Pro Pro His Gly Leu Thr Arg Thr Ser Val Thr Val Ser Asp Leu Glu
 435 440 445
 Pro His Met Asn Tyr Thr Phe Thr Val Glu Ala Arg Asn Gly Val Ser
 450 455 460
 Gly Leu Val Thr Ser Arg Ser Phe Arg Thr Ala Ser Val Ser Ile Asn
 465 470 475 480
 Gln Thr Glu Pro Pro Lys Val Arg Leu Glu Gly Arg Ser Thr Thr Ser
 485 490 495
 Leu Ser Val Ser Trp Ser Ile Pro Pro Pro Gln Gln Ser Arg Val Trp
 500 505 510
 Lys Tyr Glu Val Thr Tyr Arg Lys Lys Gly Asp Ser Asn Ser Tyr Asn
 515 520 525
 Val Arg Arg Thr Glu Gly Phe Ser Val Thr Leu Asp Asp Leu Ala Pro
 530 535 540
 Asp Thr Thr Tyr Leu Val Gln Val Gln Ala Leu Thr Gln Glu Gly Gln
 545 550 555 560
 Gly Ala Gly Ser Arg Val His Glu Phe Gln Thr Glu Gln Lys Leu Ile
 565 570 575
 Ser Glu Glu Asp Leu
 580

<210> 28
 <211> 1989
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Construct for fusion protein

<400> 28
 ggtacctcct ttgattagta tattcctatc ttaaagttac ttttatgtgg aggcattaac 60
 atttggttaat gacgtcaaaa ggatagcaag actagaataa agctataaag caagcatata 120
 atattgcggtt tcatcttttag aagcgaattt cgccaatatt ataattatca aaagagaggg 180
 gtggc aaacg gtattttggca ttattaggtt aaaaaatgta gaaggagagt gaaacccatg 240
 aaaaaaatta tgtagt tttt tattacatta atttttagtta gtttaccat tgcacaacaa 300
 acagaagcaa aagatgcaag tgcatttaat aaagaaaata gtattagtag tatggcacca 360
 ccagcaagtc caccagcaag tccaaaaaca ccaattgaaa aaaaacatgc agatggatcc 420
 gattataaag atgatgatga taaacaaggt aaagaagttg ttttattaga ttttgcagca 480
 gcaggtggtg aattaggttg gttaacacat ccatatggta aagggttgga tttaatgcaa 540

aatattatga atgatatgcc aatttatatg tatagtgttt gtaatgttat gagtggatgat	600
caagataaatt gggttacgtac aaattggggtt tatcgtgggtg aagcagaacg tattttttatt	660
gaattaaaaat ttacagttcg tgattgtaat agttttccag gtggtgcaag tagttgtaaa	720
gaaacattta atttatatta tgcagaaagt gatttagatt atggtacaaa ttttcaaaaa	780
cgtttattta caaaaattga tacaattgca ccagatgaaa ttacagttag tagtgatttt	840
gaagcacgtc atgttaaatt aaatgttgaa gaacgtagtg ttggtccatt aacacgtaaa	900
ggtttttatt tagcatttca agatattggg gcatgtgttg cattattaag tgttcgtgtt	960
tattataaaa aatgtccaga attattacaa ggtttagcac attttccaga aacaattgca	1020
ggtagtgatg caccaagttt agcaacagtt gcaggtagat gtggtgatca tgcagttgtt	1080
ccaccaggtg gtgaagaacc acgtatgcat tgtgcagttg atggtgaatg gttagttcca	1140
attggtcaat gtttatgtca agcaggttat gaaaaagttg aagatgcatg tcaagcatgt	1200
agtccaggtt tttttaaatt tgaagcaagt gaaagtccat gtttagaatg tccagaacat	1260
acattaccaa gtccagaagg tgcaacaagt tgtgaatgtg aagaaggttt ttttcgtgca	1320
ccacaagatc cagcaagtat gccatgtaca cgtccaccaa gtgcaccaca ttatttaaca	1380
gcagttggta tgggtgcaaa agttgaatta cgttggacac caccacaaga tagtgggtgg	1440
cgtgaagata ttgtttatag tgttacatgt gaacaatgtt ggccagaaag tggatgaatgt	1500
gggtccatgtg aagcaagtgt tcgttatagt gaaccaccac atgggtttaac acgtacaagt	1560
gttacagtta gtgatttaga accacatatg aattatacat ttacagttga agcacgtaat	1620
gggtgtagtg gtttagttac aagtcgtagt tttcgtacag caagtgttag tattaatcaa	1680
acagaaccac caaaagttcg tttagaaggt cgtagtacaa caagtttaag tgtagttgg	1740
agtattccac caccacaaca aagtcgtgtt tggaaatatg aagttacata tcgtaaaaaa	1800
ggtgatagta atagttataa tggtcgtcgt acagaaggtt ttagtggtac attagatgat	1860
ttagcaccag atacaacata tttagttcaa gttcaagcat taacacaaga aggtcaaggt	1920
gcaggtagtc gtgttcatga atttcaaaca gaacaaaaat taattagtga agaagattta	1980
tgagagctc	1989

<210> 29
 <211> 581
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Predicted Fusion protein

<400> 29

Met	Lys	Lys	Ile	Met	Leu	Val	Phe	Ile	Thr	Leu	Ile	Leu	Val	Ser	Leu	1	5	10	15
Pro	Ile	Ala	Gln	Gln	Thr	Glu	Ala	Lys	Asp	Ala	Ser	Ala	Phe	Asn	Lys	20	25	30	
Glu	Asn	Ser	Ile	Ser	Ser	Met	Ala	Pro	Pro	Ala	Ser	Pro	Pro	Ala	Ser	35	40	45	
Pro	Lys	Thr	Pro	Ile	Glu	Lys	Lys	His	Ala	Asp	Gly	Ser	Asp	Tyr	Lys	50	55	60	
Asp	Asp	Asp	Asp	Lys	Gln	Gly	Lys	Glu	Val	Val	Leu	Leu	Asp	Phe	Ala	65	70	75	80
Ala	Ala	Gly	Gly	Glu	Leu	Gly	Trp	Leu	Thr	His	Pro	Tyr	Gly	Lys	Gly	85	90	95	
Trp	Asp	Leu	Met	Gln	Asn	Ile	Met	Asn	Asp	Met	Pro	Ile	Tyr	Met	Tyr	100	105	110	
Ser	Val	Cys	Asn	Val	Met	Ser	Gly	Asp	Gln	Asp	Asn	Trp	Leu	Arg	Thr	115	120	125	
Asn	Trp	Val	Tyr	Arg	Gly	Glu	Ala	Glu	Arg	Ile	Phe	Ile	Glu	Leu	Lys	130	135	140	
Phe	Thr	Val	Arg	Asp	Cys	Asn	Ser	Phe	Pro	Gly	Gly	Ala	Ser	Ser	Cys	145	150	155	160
Lys	Glu	Thr	Phe	Asn	Leu	Tyr	Tyr	Ala	Glu	Ser	Asp	Leu	Asp	Tyr	Gly	165	170	175	
Thr	Asn	Phe	Gln	Lys	Arg	Leu	Phe	Thr	Lys	Ile	Asp	Thr	Ile	Ala	Pro	180	185	190	
Asp	Glu	Ile	Thr	Val	Ser	Ser	Asp	Phe	Glu	Ala	Arg	His	Val	Lys	Leu	195	200	205	
Asn	Val	Glu	Glu	Arg	Ser	Val	Gly	Pro	Leu	Thr	Arg	Lys	Gly	Phe	Tyr	210	215	220	
Leu	Ala	Phe	Gln	Asp	Ile	Gly	Ala	Cys	Val	Ala	Leu	Leu	Ser	Val	Arg	225	230	235	240
Val	Tyr	Tyr	Lys	Lys	Cys	Pro	Glu	Leu	Leu	Gln	Gly	Leu	Ala	His	Phe	245	250	255	
Pro	Glu	Thr	Ile	Ala	Gly	Ser	Asp	Ala	Pro	Ser	Leu	Ala	Thr	Val	Ala	260	265	270	
Gly	Thr	Cys	Val	Asp	His	Ala	Val	Val	Pro	Pro	Gly	Gly	Glu	Glu	Pro	275	280	285	
Arg	Met	His	Cys	Ala	Val	Asp	Gly	Glu	Trp	Leu	Val	Pro	Ile	Gly	Gln	290	295	300	
Cys	Leu	Cys	Gln	Ala	Gly	Tyr	Glu	Lys	Val	Glu	Asp	Ala	Cys	Gln	Ala	305	310	315	320
Cys	Ser	Pro	Gly	Phe	Phe	Lys	Phe	Glu	Ala	Ser	Glu	Ser	Pro	Cys	Leu				

325										330					335				
Glu	Cys	Pro	Glu	His	Thr	Leu	Pro	Ser	Pro	Glu	Gly	Ala	Thr	Ser	Cys				
			340					345					350						
Glu	Cys	Glu	Glu	Gly	Phe	Phe	Arg	Ala	Pro	Gln	Asp	Pro	Ala	Ser	Met				
		355					360					365							
Pro	Cys	Thr	Arg	Pro	Pro	Ser	Ala	Pro	His	Tyr	Leu	Thr	Ala	Val	Gly				
	370					375					380								
Met	Gly	Ala	Lys	Val	Glu	Leu	Arg	Trp	Thr	Pro	Pro	Gln	Asp	Ser	Gly				
385					390					395					400				
Gly	Arg	Glu	Asp	Ile	Val	Tyr	Ser	Val	Thr	Cys	Glu	Gln	Cys	Trp	Pro				
				405					410					415					
Glu	Ser	Gly	Glu	Cys	Gly	Pro	Cys	Glu	Ala	Ser	Val	Arg	Tyr	Ser	Glu				
			420					425					430						
Pro	Pro	His	Gly	Leu	Thr	Arg	Thr	Ser	Val	Thr	Val	Ser	Asp	Leu	Glu				
		435					440						445						
Pro	His	Met	Asn	Tyr	Thr	Phe	Thr	Val	Glu	Ala	Arg	Asn	Gly	Val	Ser				
		450				455					460								
Gly	Leu	Val	Thr	Ser	Arg	Ser	Phe	Arg	Thr	Ala	Ser	Val	Ser	Ile	Asn				
465					470					475					480				
Gln	Thr	Glu	Pro	Pro	Lys	Val	Arg	Leu	Glu	Gly	Arg	Ser	Thr	Thr	Ser				
			485						490					495					
Leu	Ser	Val	Ser	Trp	Ser	Ile	Pro	Pro	Pro	Gln	Gln	Ser	Arg	Val	Trp				
		500						505					510						
Lys	Tyr	Glu	Val	Thr	Tyr	Arg	Lys	Lys	Gly	Asp	Ser	Asn	Ser	Tyr	Asn				
		515					520					525							
Val	Arg	Arg	Thr	Glu	Gly	Phe	Ser	Val	Thr	Leu	Asp	Asp	Leu	Ala	Pro				
		530				535					540								
Asp	Thr	Thr	Tyr	Leu	Val	Gln	Val	Gln	Ala	Leu	Thr	Gln	Glu	Gly	Gln				
545				550						555					560				
Gly	Ala	Gly	Ser	Arg	Val	His	Glu	Phe	Gln	Thr	Glu	Gln	Lys	Leu	Ile				
				565					570					575					
Ser	Glu	Glu	Asp	Leu															
			580																

<210> 30

<211> 1968

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion protein construct

<400> 30

ggtacctcct ttgattagta tattcctatc ttaaagttac ttttatgtgg aggcattaac

60

atttggttaat gacgtcaaaa ggatagcaag actagaataa agctataaag caagcatata	120
atattgcggt tcatcttttag aagcgaatth cgccaatatt ataattatca aaagagaggg	180
gtggcacaacg gtatttggca ttattaggtt aaaaaatgta gaaggagagt gaaacccatg	240
gcatacgaca gtcgttttga tgaatgggta cagaaactga aagaggaaaag ctttcaaaac	300
aatacgtttg accgccgcaa atttattcaa ggagcgggga agattgcagg actttctctt	360
ggattaacga ttgccagtc ggttggggcc tttggatccg attataaaga tgatgatgat	420
aaacaaggta aagaagttgt tttattagat tttgcagcag caggtggtga attaggttgg	480
ttaacacatc catatggtaa aggttgggat ttaatgcaa atattatgaa tgatatgcca	540
atttatatgt atagtgttg taatgttatg agtggatgac aagataattg gttacgtaca	600
aattgggttt atcgtggtga agcagaacgt atttttattg aattaaaatt tacagttcgt	660
gattgtaata gttttccagg tggcgcaagt agttgtaaag aaacatttaa tttatattat	720
gcagaaagtg atttagatta tggtaaaaat tttcaaaaac gtttatttac aaaaattgat	780
acaattgcac cagatgaaat tacagttagt agtgattttg aagcacgtca tgtaaatta	840
aatgttgaag aacgtagtgt tggccatta acacgtaaag gtttttattt agcatttcaa	900
gatattggtg catgtgttgc attattaagt gttcgtgttt attataaaaa atgtccagaa	960
ttattacaag gtttagcaca tttccagaa acaattgcag gtagtgatgc accaagttta	1020
gcaacagttg caggtacatg tgttgatcat gcagttgttc caccaggtgg tgaagaacca	1080
cgtatgcatt gtgcagttga tggggaatgg ttagttccaa ttggtcaatg tttatgtcaa	1140
gcaggttatg aaaaagttga agatgcatgt caagcatgta gtccagggtt ttttaaattt	1200
gaagcaagtg aaagtccatg tttagaatgt ccagaacata cattaccaag tccagaaggt	1260
gcaacaagtt gtgaatgtga agaaggtttt tttcgtgcac cacaagatcc agcaagtatg	1320
ccatgtacac gtccaccaag tgcaccacat tatttaacag cagttggtat gggcgcaaaa	1380
gttgaattac gttggacacc accacaagat agtgggtggtc gtgaagatat tgtttatagt	1440
gttacatgtg aacaatgttg gccagaaagt ggtgaatgtg gtccatgtga agcaagtgtt	1500
cgttatagtg aaccaccaca tggtttaaca cgtacaagtg ttacagttag tgatttagaa	1560
ccacatatga attatacatt tacagttgaa gcacgtaatg gtgttagtgg tttagttaca	1620
agtcgtagtt ttcgtacagc aagtgttagt attaatacaa cagaaccacc aaaagttcgt	1680
ttagaaggtc gtagtacaac aagtttaagt gttagttgga gtattccacc accacaacaa	1740
agtcgtgttt ggaaatatga agttacatat cgtaaaaaag gtgatagtaa tagttataat	1800
gttcgtcgta cagaagggtt tagtgttaca ttagatgatt tagcaccaga tacaacatat	1860

Glu Leu Leu Gln Gly Leu Ala His Phe Pro Glu Thr Ile Ala Gly Ser
 245 250 255
 Asp Ala Pro Ser Leu Ala Thr Val Ala Gly Thr Cys Val Asp His Ala
 260 265 270
 Val Val Pro Pro Gly Gly Glu Glu Pro Arg Met His Cys Ala Val Asp
 275 280 285
 Gly Glu Trp Leu Val Pro Ile Gly Gln Cys Leu Cys Gln Ala Gly Tyr
 290 295 300
 Glu Lys Val Glu Asp Ala Cys Gln Ala Cys Ser Pro Gly Phe Phe Lys
 305 310 315 320
 Phe Glu Ala Ser Glu Ser Pro Cys Leu Glu Cys Pro Glu His Thr Leu
 325 330 335
 Pro Ser Pro Glu Gly Ala Thr Ser Cys Glu Cys Glu Glu Gly Phe Phe
 340 345 350
 Arg Ala Pro Gln Asp Pro Ala Ser Met Pro Cys Thr Arg Pro Pro Ser
 355 360 365
 Ala Pro His Tyr Leu Thr Ala Val Gly Met Gly Ala Lys Val Glu Leu
 370 375 380
 Arg Trp Thr Pro Pro Gln Asp Ser Gly Gly Arg Glu Asp Ile Val Tyr
 385 390 395 400
 Ser Val Thr Cys Glu Gln Cys Trp Pro Glu Ser Gly Glu Cys Gly Pro
 405 410 415
 Cys Glu Ala Ser Val Arg Tyr Ser Glu Pro Pro His Gly Leu Thr Arg
 420 425 430
 Thr Ser Val Thr Val Ser Asp Leu Glu Pro His Met Asn Tyr Thr Phe
 435 440 445
 Thr Val Glu Ala Arg Asn Gly Val Ser Gly Leu Val Thr Ser Arg Ser
 450 455 460
 Phe Arg Thr Ala Ser Val Ser Ile Asn Gln Thr Glu Pro Pro Lys Val
 465 470 475 480
 Arg Leu Glu Gly Arg Ser Thr Thr Ser Leu Ser Val Ser Trp Ser Ile
 485 490 495
 Pro Pro Pro Gln Gln Ser Arg Val Trp Lys Tyr Glu Val Thr Tyr Arg
 500 505 510
 Lys Lys Gly Asp Ser Asn Ser Tyr Asn Val Arg Arg Thr Glu Gly Phe
 515 520 525
 Ser Val Thr Leu Asp Asp Leu Ala Pro Asp Thr Thr Tyr Leu Val Gln
 530 535 540
 Val Gln Ala Leu Thr Gln Glu Gly Gln Gly Ala Gly Ser Arg Val His
 545 550 555 560
 Glu Phe Gln Thr Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu

565

570

<210> 32
 <211> 1254
 <212> DNA
 <213> Homo sapiens

<400> 32
 caccgcagga ggaagaacca gcgtgcccgc cagtccccgg aggacgttta cttctccaag 60
 tcagaacaac tgaagcccct gaagacatac gtggaccccc acacatatga ggacccaac 120
 caggctgtgt tgaagtccac taccgagatc catccatcct gtgtcactcg gcagaaggtg 180
 atcggagcag gagagtttgg ggaggtgtac aagggcacgc tgaagacatc ctcggggaag 240
 aaggaggtgc cgttgcccat caagacgctg aaagccggct acacagagaa gcagcgagtg 300
 gacttcctcg gcgaggccgg catcatgggc cagttcagcc accacaacat catccgccta 360
 gagggcgtca tctccaaata caagcccatg atgatcatca ctgagtacat ggagaatggg 420
 gccctggaca agttccttcg ggagaaggat ggcgagttca gcgtgctgca gctgggtggg 480
 atgctgcggg gcacgcagc tggcatgaag tacctggcca acatgaacta tgtgcaccgt 540
 gacctggctg cccgcaacat cctcgtcaac agcaacctgg tctgcaagggt gtctgacttt 600
 ggctgtccc gcgtgctgga ggacgacccc gagggcacct acaccaccag tggcggcaag 660
 atccccatcc gctggaccgc cccggaggcc atttctacc ggaagtccac ctctgccagc 720
 gacgtgtgga gctttggcat tgtcatgtgg gaggtgatga cctatggcga gcggccctac 780
 tgggagttgt ccaaccacga ggtgatgaaa gccatcaatg atggcttccg gctccccaca 840
 cccatggact gccctccgc catctaccag ctcatgatgc agtgctggca gcaggagcgt 900
 gcccgcgcc ccaagttcgc tgacatcgtc agcatcctgg acaagctcat tcgtgccctt 960
 gactccctca agaccctggc tgactttgac ccccgctgtg ctatccggct cccagcacg 1020
 agcggtcgg agggggtgcc cttccgcacg gtgtccgagt ggctggagtc catcaagatg 1080
 cagcagtata cggagcactt catggcggcc ggctacactg ccatcgagaa ggtggtgcag 1140
 atgaccaacg acgacatcaa gaggattggg gtgcggctgc ccggccacca gaagcgcac 1200
 gcctacagcc tgctgggact caaggaccag gtgaacactg tggggatccc catc 1254

<210> 33
 <211> 1254
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Sequence Optimized for codon usage in Listeria

<400> 33
cacagacgta gaaaaaatca acgtgctcga caatccccag aagatgtgta tttttcgaaa 60
agtgaacaat taaaaccatt aaaaacttat gttgatccgc atacgtacga agacccaaat 120
caagcagtat taaaattttac aacagaaata caccgaagtt gtgtttacaag acaaaaagtt 180
attggagcag gtgaattcgg agaggtatat aaaggtatgt taaaaacatc atcaggtaaa 240
aaagaagttc cggttgcaat taaaacctta aaggcaggat atacagaaaa acagcgagtt 300
gatttttttag gtgaagcagg aattatgggt caatttagcc atcataatat tattcgtttg 360
gaaggagtaa taagtaaata taaaccaatg atgattatta cagaatacat ggaaaacggt 420
gcttttagata aattttttacg tgaaaaggat ggtgaattta gtgtttttaca attggttggt 480
atgttaagag gaattgctgc aggtatgaaa tatttagcta atatgaatta tgttcaccgt 540
gatttggcag caagaaatat cctagtcaat tccaatttag tatgtaaagt tagtgatttt 600
ggtttaagca gagtattaga agacgatcca gaggcaacct atacaacatc gggaggtaaa 660
attcctattc gttggacagc accagaagct atcagttacc gttaaatttac aagtgcacat 720
gacgtgtgga gttttgggat tgtaatgtgg gaagttatga catatggaga aagaccatat 780
tggaattaa gtaatcatga agttatgaaa gcaattaacg atggatttag attaccaact 840
ccgatggatt gtccatctgc catttatcaa ctaatgatgc aatgttggca acaagaaaga 900
gcacgacgtc caaaatttgc agatattggt agtatttttag acaaattaat tcgtgcacca 960
gatagtttaa aaacttttagc agactttgat cctcgtgtta gtattcgatt accaagtacg 1020
tcaggttccg aaggagttcc atttcgcaca gtctccgaat ggttggaatc aattaaatg 1080
caacaatata ccgaacactt tatggcagca ggttacacag caatcgaaaa agttgttcaa 1140
atgacaaatg atgatattaa acgtattgga gtttagattac caggccacca gaaacgtatt 1200
gcatattcctt tatttaggttt aaaagatcaa gttaataccg tgggaattcc aatt 1254

<210> 34
<211> 456
<212> PRT
<213> Homo sapiens

<400> 34

Val	His	Glu	Phe	Gln	Thr	Leu	Ser	Pro	Glu	Gly	Ser	Gly	Asn	Leu	Ala
1				5				10						15	
Val	Ile	Gly	Gly	Val	Ala	Val	Gly	Val	Val	Leu	Leu	Leu	Val	Leu	Ala
			20					25					30		
Gly	Val	Gly	Phe	Phe	Ile	His	Arg	Arg	Arg	Lys	Asn	Gln	Arg	Ala	Arg
		35					40				45				
Gln	Ser	Pro	Glu	Asp	Val	Tyr	Phe	Ser	Lys	Ser	Glu	Gln	Leu	Lys	Pro

50					55					60					
Leu	Lys	Thr	Tyr	Val	Asp	Pro	His	Thr	Tyr	Glu	Asp	Pro	Asn	Gln	Ala
65					70					75					80
Val	Leu	Lys	Phe	Thr	Thr	Glu	Ile	His	Pro	Ser	Cys	Val	Thr	Arg	Gln
				85					90					95	
Lys	Val	Ile	Gly	Ala	Gly	Glu	Phe	Gly	Glu	Val	Tyr	Lys	Gly	Met	Leu
			100					105					110		
Lys	Thr	Ser	Ser	Gly	Lys	Lys	Glu	Val	Pro	Val	Ala	Ile	Lys	Thr	Leu
		115					120					125			
Lys	Ala	Gly	Tyr	Thr	Glu	Lys	Gln	Arg	Val	Asp	Phe	Leu	Gly	Glu	Ala
	130					135					140				
Gly	Ile	Met	Gly	Gln	Phe	Ser	His	His	Asn	Ile	Ile	Arg	Leu	Glu	Gly
145					150				155					160	
Val	Ile	Ser	Lys	Tyr	Lys	Pro	Met	Met	Ile	Ile	Thr	Glu	Tyr	Met	Glu
				165					170					175	
Asn	Gly	Ala	Leu	Asp	Lys	Phe	Leu	Arg	Glu	Lys	Asp	Gly	Glu	Phe	Ser
			180					185					190		
Val	Leu	Gln	Leu	Val	Gly	Met	Leu	Arg	Gly	Ile	Ala	Ala	Gly	Met	Lys
		195					200					205			
Tyr	Leu	Ala	Asn	Met	Asn	Tyr	Val	His	Arg	Asp	Leu	Ala	Ala	Arg	Asn
	210					215					220				
Ile	Leu	Val	Asn	Ser	Asn	Leu	Val	Cys	Lys	Val	Ser	Asp	Phe	Gly	Leu
225						230					235				240
Ser	Arg	Val	Leu	Glu	Asp	Asp	Pro	Glu	Ala	Thr	Tyr	Thr	Thr	Ser	Gly
				245					250					255	
Gly	Lys	Ile	Pro	Ile	Arg	Trp	Thr	Ala	Pro	Glu	Ala	Ile	Ser	Tyr	Arg
			260					265					270		
Lys	Phe	Thr	Ser	Ala	Ser	Asp	Val	Trp	Ser	Phe	Gly	Ile	Val	Met	Trp
		275					280					285			
Glu	Val	Met	Thr	Tyr	Gly	Glu	Arg	Pro	Tyr	Trp	Glu	Leu	Ser	Asn	His
	290					295					300				
Glu	Val	Met	Lys	Ala	Ile	Asn	Asp	Gly	Phe	Arg	Leu	Pro	Thr	Pro	Met
305					310					315					320
Asp	Cys	Pro	Ser	Ala	Ile	Tyr	Gln	Leu	Met	Met	Gln	Cys	Trp	Gln	Gln
				325					330					335	
Glu	Arg	Ala	Arg	Arg	Pro	Lys	Phe	Ala	Asp	Ile	Val	Ser	Ile	Leu	Asp
			340					345					350		
Lys	Leu	Ile	Arg	Ala	Pro	Asp	Ser	Leu	Lys	Thr	Leu	Ala	Asp	Phe	Asp
		355					360					365			
Pro	Arg	Val	Ser	Ile	Arg	Leu	Pro	Ser	Thr	Ser	Gly	Ser	Glu	Gly	Val
	370					375					380				

Pro Phe Arg Thr Val Ser Glu Trp Leu Glu Ser Ile Lys Met Gln Gln
385 390 395 400

Tyr Thr Glu His Phe Met Ala Ala Gly Tyr Thr Ala Ile Glu Lys Val
405 410 415

Val Gln Met Thr Asn Asp Asp Ile Lys Arg Ile Gly Val Arg Leu Pro
420 425 430

Gly His Gln Lys Arg Ile Ala Tyr Ser Leu Leu Gly Leu Lys Asp Gln
435 440 445

Val Asn Thr Val Gly Ile Pro Ile
450 455

<210> 35
<211> 1437
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Fusion Protein

<400> 35
atgaaaaaaaa taatgctagt ttttattaca cttatattag ttagtctacc aattgcgcaa 60
caaaactgaag caaaggatgc atctgcattc aataaagaaa attcaatttc atccatggca 120
ccaccagcat ctccgcctgc aagtcctaag acgccaatcg aaaagaaaca cgcggatctc 180
gagcaccgca ggaggaagaa ccagcgtgcc cgccagtcctc cggaggacgt ttacttctcc 240
aagtcagaac aactgaagcc cctgaagaca tacgtggacc cccacacata tgaggacccc 300
aaccaggctg tggtgaagtt cactaccgag atccatccat cctgtgtcac tcggcagaag 360
gtgatcggag caggagagtt tggggaggtg tacaagggca tgctgaagac atcctcgggg 420
aagaaggagg tgccggtggc catcaagacg ctgaaagccg gctacacaga gaagcagcga 480
gtggacttcc tcggcgaggc cggcatcatg ggccagttca gccaccacaa catcatccgc 540
ctagagggcg tcatctccaa atacaagccc atgatgatca tcaactgagta catggagaat 600
ggggccctgg acaagttcct tcgggagaag gatggcgagt tcagcgtgct gcagctgggtg 660
ggcatgctgc ggggcatcgc agctggcatg aagtacctgg ccaacatgaa ctatgtgcac 720
cgtgacctgg ctgcccgcga catcctcgtc aacagcaacc tgggtctgcaa ggtgtctgac 780
tttggcctgt cccgcgtgct ggaggacgac cccgaggcca cctacaccac cagtggcggc 840
aagatcccca tccgctggac cgccccggag gccatttcct accggaagtt cacctctgcc 900
agcgacgtgt ggagcttttg cattgtcatg tgggaggtga tgacctatgg cgagcggccc 960
tactgggagt tgtccaacca cgaggtgatg aaagccatca atgatggctt ccggctcccc 1020
acacccatgg actgcccctc cgccatctac cagctcatga tgcagtgtg gcagcaggag 1080

```

cgtgcccgcc gccccaagtt cgctgacatc gtcagcatcc tggacaagct cattcgtgcc 1140
cctgactccc tcaagaccct ggctgacttt gacccccgcg tgtctatccg gctccccagc 1200
acgagcgggt cggaggggggt gcccttccgc acggtgtccg agtgggtgga gtccatcaag 1260
atgcagcagt atacggagca cttcatggcg gccggctaca ctgccatcga gaaggtgggtg 1320
cagatgacca acgacgacat caagaggatt ggggtgcggc tgcccggcca ccagaagcgc 1380
atcgctaca gcctgctggg actcaaggac caggtgaaca ctgtggggat ccccatc 1437

```

<210> 36

<211> 479

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Predicted Protein Sequence

<400> 36

```

Met Lys Lys Ile Met Leu Val Phe Ile Thr Leu Ile Leu Val Ser Leu
1             5             10             15
Pro Ile Ala Gln Gln Thr Glu Ala Lys Asp Ala Ser Ala Phe Asn Lys
                20             25             30
Glu Asn Ser Ile Ser Ser Met Ala Pro Pro Ala Ser Pro Pro Ala Ser
                35             40             45
Pro Lys Thr Pro Ile Glu Lys Lys His Ala Asp Leu Glu His Arg Arg
                50             55             60
Arg Lys Asn Gln Arg Ala Arg Gln Ser Pro Glu Asp Val Tyr Phe Ser
        65             70             75             80
Lys Ser Glu Gln Leu Lys Pro Leu Lys Thr Tyr Val Asp Pro His Thr
                85             90             95
Tyr Glu Asp Pro Asn Gln Ala Val Leu Lys Phe Thr Thr Glu Ile His
                100            105            110
Pro Ser Cys Val Thr Arg Gln Lys Val Ile Gly Ala Gly Glu Phe Gly
        115            120            125
Glu Val Tyr Lys Gly Met Leu Lys Thr Ser Ser Gly Lys Lys Glu Val
        130            135            140
Pro Val Ala Ile Lys Thr Leu Lys Ala Gly Tyr Thr Glu Lys Gln Arg
        145            150            155            160
Val Asp Phe Leu Gly Glu Ala Gly Ile Met Gly Gln Phe Ser His His
                165            170            175
Asn Ile Ile Arg Leu Glu Gly Val Ile Ser Lys Tyr Lys Pro Met Met
        180            185            190
Ile Ile Thr Glu Tyr Met Glu Asn Gly Ala Leu Asp Lys Phe Leu Arg

```

195					200					205					
Glu	Lys	Asp	Gly	Glu	Phe	Ser	Val	Leu	Gln	Leu	Val	Gly	Met	Leu	Arg
210						215					220				
Gly	Ile	Ala	Ala	Gly	Met	Lys	Tyr	Leu	Ala	Asn	Met	Asn	Tyr	Val	His
225					230					235					240
Arg	Asp	Leu	Ala	Ala	Arg	Asn	Ile	Leu	Val	Asn	Ser	Asn	Leu	Val	Cys
				245					250					255	
Lys	Val	Ser	Asp	Phe	Gly	Leu	Ser	Arg	Val	Leu	Glu	Asp	Asp	Pro	Glu
			260					265					270		
Ala	Thr	Tyr	Thr	Thr	Ser	Gly	Gly	Lys	Ile	Pro	Ile	Arg	Trp	Thr	Ala
			275				280					285			
Pro	Glu	Ala	Ile	Ser	Tyr	Arg	Lys	Phe	Thr	Ser	Ala	Ser	Asp	Val	Trp
	290					295					300				
Ser	Phe	Gly	Ile	Val	Met	Trp	Glu	Val	Met	Thr	Tyr	Gly	Glu	Arg	Pro
305					310					315					320
Tyr	Trp	Glu	Leu	Ser	Asn	His	Glu	Val	Met	Lys	Ala	Ile	Asn	Asp	Gly
				325					330					335	
Phe	Arg	Leu	Pro	Thr	Pro	Met	Asp	Cys	Pro	Ser	Ala	Ile	Tyr	Gln	Leu
			340					345					350		
Met	Met	Gln	Cys	Trp	Gln	Gln	Glu	Arg	Ala	Arg	Arg	Pro	Lys	Phe	Ala
		355					360					365			
Asp	Ile	Val	Ser	Ile	Leu	Asp	Lys	Leu	Ile	Arg	Ala	Pro	Asp	Ser	Leu
	370					375					380				
Lys	Thr	Leu	Ala	Asp	Phe	Asp	Pro	Arg	Val	Ser	Ile	Arg	Leu	Pro	Ser
385					390					395				400	
Thr	Ser	Gly	Ser	Glu	Gly	Val	Pro	Phe	Arg	Thr	Val	Ser	Glu	Trp	Leu
				405					410					415	
Glu	Ser	Ile	Lys	Met	Gln	Gln	Tyr	Thr	Glu	His	Phe	Met	Ala	Ala	Gly
			420					425					430		
Tyr	Thr	Ala	Ile	Glu	Lys	Val	Val	Gln	Met	Thr	Asn	Asp	Asp	Ile	Lys
		435					440					445			
Arg	Ile	Gly	Val	Arg	Leu	Pro	Gly	His	Gln	Lys	Arg	Ile	Ala	Tyr	Ser
	450					455					460				
Leu	Leu	Gly	Leu	Lys	Asp	Gln	Val	Asn	Thr	Val	Gly	Ile	Pro	Ile	
465					470					475					

<210> 37

<211> 1737

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion protein sequence

<400> 37

ggtacctcct ttgattagta tattcctatc ttaaagttac ttttatgtgg aggcattaac	60
at ttgttaat gacgtcaaaa ggatagcaag actagaataa agctataaag caagcatata	120
atattgcggt tcatcttttag aagcgaattt cgccaatatt ataattatca aaagagaggg	180
gtggcaaacg gtat ttggca ttattaggtt aaaaaatgta gaaggagagt gaaacccatg	240
aaaaaaataa tgctagtttt tattacactt atattagtta gtctaccaat tgcgcaacaa	300
actgaagcaa aggatgcatc tgcattcaat aaagaaaatt caatttcatc catggcacca	360
ccagcatctc cgcctgcaag tcctaagacg ccaatcgaaa agaaacacgc ggatggatcc	420
gattataaag atgatgatga taaacacaga cgtagaaaaa atcaacgtgc tcgacaatcc	480
ccagaagatg tgtat ttttc gaaaagtga caattaaaac cattaaaaac ttatgttgat	540
ccgcatacgt acgaagaccc aaatcaagca gtattaaaat ttacaacaga aatacaccca	600
agttgtgtta caagacaaaa agttattgga gcaggtgaat tcggagaggt atataaaggt	660
atgttaaaaa catcatcagg taaaaaagaa gttccggttg caattaaaac cttaaaggca	720
ggatatacag aaaaacacgc agttgatttt ttaggtgaag caggaattat gggatcaattt	780
agccatcata atattattcg tttggaagga gtaataagta aatataaacc aatgatgatt	840
attacagaat acatggaaaa cgggtgcttta gataaatttt tacgtgaaaa ggatggtgaa	900
tttagtgttt tacaattggt tggtatgtta agaggaattg ctgcagggtat gaaatattta	960
gctaatatga attatgttca ccgtgatttg gcagcaagaa atatcctagt caattccaat	1020
ttagtatgta aagttagtga ttttggttta agcagagtat tagaagacga tccagaggca	1080
acctatacaa catcgggagg taaaattcct attcgttgga cagcaccaga agctatcagt	1140
taccgtaaat ttacaagtgc atcagacgtg tggagttttg ggattgtaat gtgggaagtt	1200
atgacatatg gagaaagacc atattgggaa ttaagtaatc atgaagtat gaaagcaatt	1260
aacgatggat ttagattacc aactccgatg gattgtccat ctgccattta tcaactaatg	1320
atgcaatggt ggcaacaaga aagagcacga cgtccaaaat ttgcagatat tgttagtatt	1380
ttagacaaat taattcgtgc accagatagt ttaaaaactt tagcagactt tgatcctcgt	1440
gtagtat ttc gattaccaag tacgtcaggt tccgaaggag ttccatttcg cacagtctcc	1500
gaatggtttg aatcaattaa aatgcaacaa tacaccgaac actttatggc agcaggttac	1560
acagcaatcg aaaaagttgt tcaaatgaca aatgatgata ttaaacgtat tggagttaga	1620
ttaccaggcc accagaaacg tattgcatat tctttattag gtttaaaaga tcaagttaat	1680
accgtgggaa ttccaattga acaaaaatta atttccgaag aagacttata agagctc	1737

<210> 38
 <211> 497
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Predicted fusion protein

 <400> 38

 Met Lys Lys Ile Met Leu Val Phe Ile Thr Leu Ile Leu Val Ser Leu
 1 5 10 15
 Pro Ile Ala Gln Gln Thr Glu Ala Lys Asp Ala Ser Ala Phe Asn Lys
 20 25 30
 Glu Asn Ser Ile Ser Ser Met Ala Pro Pro Ala Ser Pro Pro Ala Ser
 35 40 45
 Pro Lys Thr Pro Ile Glu Lys Lys His Ala Asp Gly Ser Asp Tyr Lys
 50 55 60
 Asp Asp Asp Asp Lys His Arg Arg Arg Lys Asn Gln Arg Ala Arg Gln
 65 70 75 80
 Ser Pro Glu Asp Val Tyr Phe Ser Lys Ser Glu Gln Leu Lys Pro Leu
 85 90 95
 Lys Thr Tyr Val Asp Pro His Thr Tyr Glu Asp Pro Asn Gln Ala Val
 100 105 110
 Leu Lys Phe Thr Thr Glu Ile His Pro Ser Cys Val Thr Arg Gln Lys
 115 120 125
 Val Ile Gly Ala Gly Glu Phe Gly Glu Val Tyr Lys Gly Met Leu Lys
 130 135 140
 Thr Ser Ser Gly Lys Lys Glu Val Pro Val Ala Ile Lys Thr Leu Lys
 145 150 155 160
 Ala Gly Tyr Thr Glu Lys Gln Arg Val Asp Phe Leu Gly Glu Ala Gly
 165 170 175
 Ile Met Gly Gln Phe Ser His His Asn Ile Ile Arg Leu Glu Gly Val
 180 185 190
 Ile Ser Lys Tyr Lys Pro Met Met Ile Ile Thr Glu Tyr Met Glu Asn
 195 200 205
 Gly Ala Leu Asp Lys Phe Leu Arg Glu Lys Asp Gly Glu Phe Ser Val
 210 215 220
 Leu Gln Leu Val Gly Met Leu Arg Gly Ile Ala Ala Gly Met Lys Tyr
 225 230 235 240
 Leu Ala Asn Met Asn Tyr Val His Arg Asp Leu Ala Ala Arg Asn Ile
 245 250 255
 Leu Val Asn Ser Asn Leu Val Cys Lys Val Ser Asp Phe Gly Leu Ser
 260 265 270

Arg Val Leu Glu Asp Asp Pro Glu Ala Thr Tyr Thr Thr Ser Gly Gly
 275 280 285
 Lys Ile Pro Ile Arg Trp Thr Ala Pro Glu Ala Ile Ser Tyr Arg Lys
 290 295 300
 Phe Thr Ser Ala Ser Asp Val Trp Ser Phe Gly Ile Val Met Trp Glu
 305 310 315 320
 Val Met Thr Tyr Gly Glu Arg Pro Tyr Trp Glu Leu Ser Asn His Glu
 325 330 335
 Val Met Lys Ala Ile Asn Asp Gly Phe Arg Leu Pro Thr Pro Met Asp
 340 345 350
 Cys Pro Ser Ala Ile Tyr Gln Leu Met Met Gln Cys Trp Gln Gln Glu
 355 360 365
 Arg Ala Arg Arg Pro Lys Phe Ala Asp Ile Val Ser Ile Leu Asp Lys
 370 375 380
 Leu Ile Arg Ala Pro Asp Ser Leu Lys Thr Leu Ala Asp Phe Asp Pro
 385 390 395 400
 Arg Val Ser Ile Arg Leu Pro Ser Thr Ser Gly Ser Glu Gly Val Pro
 405 410 415
 Phe Arg Thr Val Ser Glu Trp Leu Glu Ser Ile Lys Met Gln Gln Tyr
 420 425 430
 Thr Glu His Phe Met Ala Ala Gly Tyr Thr Ala Ile Glu Lys Val Val
 435 440 445
 Gln Met Thr Asn Asp Asp Ile Lys Arg Ile Gly Val Arg Leu Pro Gly
 450 455 460
 His Gln Lys Arg Ile Ala Tyr Ser Leu Leu Gly Leu Lys Asp Gln Val
 465 470 475 480
 Asn Thr Val Gly Ile Pro Ile Glu Gln Lys Leu Ile Ser Glu Glu Asp
 485 490 495

Leu

<210> 39

<211> 1737

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion protein construct

<400> 39

ggtagcctcct ttgattagta tattcctatc ttaaagttac ttttatgtgg aggcattaac 60

atttggttaat gacgtcaaaa ggatagcaag actagaataa agctataaag caagcatata 120

atattgcggtt tcatcttttag aagcgaattt cgccaatatt ataattatca aaagagaggg 180

gtggcaaacg gtatttggca ttattaggtt aaaaaatgta gaaggagagt gaaacccatg	240
aaaaaaatta tgttagtttt tattacatta attttagtta gtttaccaat tgcacaacaa	300
acagaagcaa aagatgcaag tgcatttaat aaagaaaata gtattagtag tatggcacca	360
ccagcaagtc caccagcaag tccaaaaaca ccaattgaaa aaaaacatgc agatggatcc	420
gattataaag acgatgatga taaacacaga cgtagaaaaa atcaacgtgc tcgacaatcc	480
ccagaagatg tgtatttttc gaaaagtga caattaaaac cattaataaac ttatgttgat	540
cgcatacgt acgaagaccc aatcaagca gtattaaaat ttacaacaga aatacaccca	600
agttgtgtta caagacaaaa agttattgga gcaggtgaat tcggagaggt atataaaggt	660
atgttaaaaa catcatcagg taaaaaagaa gttccggttg caattaaaac cttaaaggca	720
ggatatacag aaaaacagcg agttgatttt ttaggtgaag caggaattat gggatcaattt	780
agccatcata atattattcg tttggaagga gtaataagta aatataaacc aatgatgatt	840
attacagaat acatggaaaa cggtgcttta gataaatttt tacgtgaaaa ggatggtgaa	900
tttagtgttt tacaattggg ttggtatgta agaggaattg ctgcaggtat gaaatattta	960
gctaatatga attatgttca ccgtgatttg gcagcaagaa ataccctagt caattccaat	1020
ttagtatgta aagttagtga ttttggttta agcagagtat tagaagacga tccagaggca	1080
acctatacaa catcgggagg taaaattcct attcgttgga cagcaccaga agctatcagt	1140
taccgtaaat ttacaagtgc atcagacgtg tggagttttg ggattgtaat gtgggaagtt	1200
atgacatatg gagaaagacc atattgggaa ttaagtaatc atgaagttat gaaagcaatt	1260
aacgatggat ttagattacc aactccgatg gattgtccat ctgccattta tcaactaatg	1320
atgcaatggt ggcaacaaga aagagcacga cgtccaaaat ttgcagatat tgttagtatt	1380
ttagacaaat taattcgtgc accagatagt ttaaaaactt tagcagactt tgatcctcgt	1440
gtagtatatt gattaccaag tacgtcaggt tccgaaggag ttccatttcg cacagtctcc	1500
gaatggtttg aatcaattaa aatgcaacaa tacaccgaac actttatggc agcaggttac	1560
acagcaatcg aaaaagttgt tcaaatgaca aatgatgata ttaaactgat tggagttaga	1620
ttaccaggcc accagaaacg tattgcatat tctttattag gtttaaaaga tcaagttaat	1680
accgtgggaa ttccaattga aaaaaatta atttccgaag aagacttata agagctc	1737

<210> 40

<211> 497

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Predicted Fusion Protein

<400> 40

Met	Lys	Lys	Ile	Met	Leu	Val	Phe	Ile	Thr	Leu	Ile	Leu	Val	Ser	Leu	1	5	10	15
Pro	Ile	Ala	Gln	Gln	Thr	Glu	Ala	Lys	Asp	Ala	Ser	Ala	Phe	Asn	Lys	20	25	30	
Glu	Asn	Ser	Ile	Ser	Ser	Met	Ala	Pro	Pro	Ala	Ser	Pro	Pro	Ala	Ser	35	40	45	
Pro	Lys	Thr	Pro	Ile	Glu	Lys	Lys	His	Ala	Asp	Gly	Ser	Asp	Tyr	Lys	50	55	60	
Asp	Asp	Asp	Asp	Lys	His	Arg	Arg	Arg	Lys	Asn	Gln	Arg	Ala	Arg	Gln	5	70	75	80
Ser	Pro	Glu	Asp	Val	Tyr	Phe	Ser	Lys	Ser	Glu	Gln	Leu	Lys	Pro	Leu	85	90	95	
Lys	Thr	Tyr	Val	Asp	Pro	His	Thr	Tyr	Glu	Asp	Pro	Asn	Gln	Ala	Val	100	105	110	
Leu	Lys	Phe	Thr	Thr	Glu	Ile	His	Pro	Ser	Cys	Val	Thr	Arg	Gln	Lys	115	120	125	
Val	Ile	Gly	Ala	Gly	Glu	Phe	Gly	Glu	Val	Tyr	Lys	Gly	Met	Leu	Lys	130	135	140	
Thr	Ser	Ser	Gly	Lys	Lys	Glu	Val	Pro	Val	Ala	Ile	Lys	Thr	Leu	Lys	145	150	155	160
Ala	Gly	Tyr	Thr	Glu	Lys	Gln	Arg	Val	Asp	Phe	Leu	Gly	Glu	Ala	Gly	165	170	175	
Ile	Met	Gly	Gln	Phe	Ser	His	His	Asn	Ile	Ile	Arg	Leu	Glu	Gly	Val	180	185	190	
Ile	Ser	Lys	Tyr	Lys	Pro	Met	Met	Ile	Ile	Thr	Glu	Tyr	Met	Glu	Asn	195	200	205	
Gly	Ala	Leu	Asp	Lys	Phe	Leu	Arg	Glu	Lys	Asp	Gly	Glu	Phe	Ser	Val	210	215	220	
Leu	Gln	Leu	Val	Gly	Met	Leu	Arg	Gly	Ile	Ala	Ala	Gly	Met	Lys	Tyr	225	230	235	240
Leu	Ala	Asn	Met	Asn	Tyr	Val	His	Arg	Asp	Leu	Ala	Ala	Arg	Asn	Ile	245	250	255	
Leu	Val	Asn	Ser	Asn	Leu	Val	Cys	Lys	Val	Ser	Asp	Phe	Gly	Leu	Ser	260	265	270	
Arg	Val	Leu	Glu	Asp	Asp	Pro	Glu	Ala	Thr	Tyr	Thr	Thr	Ser	Gly	Gly	275	280	285	
Lys	Ile	Pro	Ile	Arg	Trp	Thr	Ala	Pro	Glu	Ala	Ile	Ser	Tyr	Arg	Lys	290	295	300	
Phe	Thr	Ser	Ala	Ser	Asp	Val	Trp	Ser	Phe	Gly	Ile	Val	Met	Trp	Glu	305	310	315	320

Val Met Thr Tyr Gly Glu Arg Pro Tyr Trp Glu Leu Ser Asn His Glu
325 330 335

Val Met Lys Ala Ile Asn Asp Gly Phe Arg Leu Pro Thr Pro Met Asp
340 345 350

Cys Pro Ser Ala Ile Tyr Gln Leu Met Met Gln Cys Trp Gln Gln Glu
355 360 365

Arg Ala Arg Arg Pro Lys Phe Ala Asp Ile Val Ser Ile Leu Asp Lys
370 375 380

Leu Ile Arg Ala Pro Asp Ser Leu Lys Thr Leu Ala Asp Phe Asp Pro
385 390 395 400

Arg Val Ser Ile Arg Leu Pro Ser Thr Ser Gly Ser Glu Gly Val Pro
405 410 415

Phe Arg Thr Val Ser Glu Trp Leu Glu Ser Ile Lys Met Gln Gln Tyr
420 425 430

Thr Glu His Phe Met Ala Ala Gly Tyr Thr Ala Ile Glu Lys Val Val
435 440 445

Gln Met Thr Asn Asp Asp Ile Lys Arg Ile Gly Val Arg Leu Pro Gly
450 455 460

His Gln Lys Arg Ile Ala Tyr Ser Leu Leu Gly Leu Lys Asp Gln Val
465 470 475 480

Asn Thr Val Gly Ile Pro Ile Glu Gln Lys Leu Ile Ser Glu Glu Asp
485 490 495

Leu

<210> 41
<211> 1716
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Fusion protein construct

<400> 41
ggtagctcct ttgattagta tattcctatc tttaaagttac ttttatgtgg aggcattaac 60
atttggttaat gacgtcaaaa ggatagcaag actagaataa agctataaag caagcatata 120
atattgcggtt tcattcttag aagcgaattt cgccaatatt ataattatca aaagagaggg 180
gtggcaaacg gtatttggca ttattaggtt aaaaaatgta gaaggagagt gaaacccatg 240
gcatacgaca gtcgttttga tgaatgggta cagaaactga aagaggaaag ctttcaaaac 300
aatacgtttg accgccgcaa atttattcaa ggagcgggga agattgcagg actttctctt 360
ggattaacga ttgccagtc ggttggggcc tttggatccg attataaaga tgatgatgat 420

```

aaacacagac gtagaaaaaa tcaacgtgct cgacaatccc cagaagatgt gtatttttcg      480
aaaagtgaac aattaaaacc attaaaaact tatgttgatc cgcatacgta cgaagaccca      540
aatcaagcag tattaaaatt tacaacagaa atacacccaa gttgtgttac aagacaaaaa      600
gttattggag caggtgaatt cggagaggta tataaaggta tgttaaaaac atcatcaggt      660
aaaaaagaag ttccggttgc aattaaaacc ttaaaggcag gatatacaga aaaacagcga      720
gttgattttt taggtgaagc aggaattatg ggtcaattta gccatcataa tattattcgt      780
ttggaaggag taataagtaa atataaacca atgatgatta ttacagaata catggaaaac      840
ggtgcttttag ataaattttt acgtgaaaag gatggtgaat ttagtgtttt acaattggtt      900
ggtatgttaa gaggaattgc tgcaggtatg aaatatttag ctaatatgaa ttatgttcac      960
cgtgatttgg cagcaagaaa taccctagtc aattccaatt tagtatgtaa agttagtgat     1020
tttggtttta gcagagtatt agaagacgat ccagaggcaa cctatacaac atcgggaggt     1080
aaaattccta ttcgttggac agcaccagaa gctatcagtt accgtaaatt tacaagtgca     1140
tcagacgtgt ggagtttttg gattgtaatg tgggaagtta tgacatatgg agaaagacca     1200
tattgggaat taagtaatca tgaagttatg aaagcaatta acgatggatt tagattacca     1260
actccgatgg attgtccatc tgccatttat caactaatga tgcaatgttg gcaacaagaa     1320
agagcacgac gtccaaaatt tgcagatatt gttagtattt tagacaaatt aattcgtgca     1380
ccagatagtt taaaaacttt agcagacttt gatcctcgtg ttagtattcg attaccaagt     1440
acgtcaggtt ccgaaggagt tccatttcgc acagtctccg aatggttgga atcaattaaa     1500
atgcaacaat acaccgaaca ctttatggca gcaggttaca cagcaatcga aaaagttggt     1560
caaatgacaa atgatgatat taaacgtatt ggagttagat taccaggcca ccagaaacgt     1620
attgcatatt ctttattagg tttaaaagat caagttaata ccgtgggaat tccaattgaa     1680
caaaaattaa tttccgaaga agacttataa gagctc                                1716

```

<210> 42

<211> 490

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Predicted fusion protein

<400> 42

```

Met Ala Tyr Asp Ser Arg Phe Asp Glu Trp Val Gln Lys Leu Lys Glu
1           5           10           15

```

```

Glu Ser Phe Gln Asn Asn Thr Phe Asp Arg Arg Lys Phe Ile Gln Gly
20           25           30

```

Ala Gly Lys Ile Ala Gly Leu Ser Leu Gly Leu Thr Ile Ala Gln Ser
 35 40 45
 Val Gly Ala Phe Gly Ser Asp Tyr Lys Asp Asp Asp Lys His Arg
 50 55 60
 Arg Arg Lys Asn Gln Arg Ala Arg Gln Ser Pro Glu Asp Val Tyr Phe
 65 70 75 80
 Ser Lys Ser Glu Gln Leu Lys Pro Leu Lys Thr Tyr Val Asp Pro His
 85 90 95
 Thr Tyr Glu Asp Pro Asn Gln Ala Val Leu Lys Phe Thr Thr Glu Ile
 100 105 110
 His Pro Ser Cys Val Thr Arg Gln Lys Val Ile Gly Ala Gly Glu Phe
 115 120 125
 Gly Glu Val Tyr Lys Gly Met Leu Lys Thr Ser Ser Gly Lys Lys Glu
 130 135 140
 Val Pro Val Ala Ile Lys Thr Leu Lys Ala Gly Tyr Thr Glu Lys Gln
 145 150 155 160
 Arg Val Asp Phe Leu Gly Glu Ala Gly Ile Met Gly Gln Phe Ser His
 165 170 175
 His Asn Ile Ile Arg Leu Glu Gly Val Ile Ser Lys Tyr Lys Pro Met
 180 185 190
 Met Ile Ile Thr Glu Tyr Met Glu Asn Gly Ala Leu Asp Lys Phe Leu
 195 200 205
 Arg Glu Lys Asp Gly Glu Phe Ser Val Leu Gln Leu Val Gly Met Leu
 210 215 220
 Arg Gly Ile Ala Ala Gly Met Lys Tyr Leu Ala Asn Met Asn Tyr Val
 225 230 235 240
 His Arg Asp Leu Ala Ala Arg Asn Ile Leu Val Asn Ser Asn Leu Val
 245 250 255
 Cys Lys Val Ser Asp Phe Gly Leu Ser Arg Val Leu Glu Asp Asp Pro
 260 265 270
 Glu Ala Thr Tyr Thr Thr Ser Gly Gly Lys Ile Pro Ile Arg Trp Thr
 275 280 285
 Ala Pro Glu Ala Ile Ser Tyr Arg Lys Phe Thr Ser Ala Ser Asp Val
 290 295 300
 Trp Ser Phe Gly Ile Val Met Trp Glu Val Met Thr Tyr Gly Glu Arg
 305 310 315 320
 Pro Tyr Trp Glu Leu Ser Asn His Glu Val Met Lys Ala Ile Asn Asp
 325 330 335
 Gly Phe Arg Leu Pro Thr Pro Met Asp Cys Pro Ser Ala Ile Tyr Gln
 340 345 350
 Leu Met Met Gln Cys Trp Gln Gln Glu Arg Ala Arg Arg Pro Lys Phe

355	360	365
Ala Asp Ile Val Ser Ile Leu Asp Lys Leu Ile Arg Ala Pro Asp Ser		
370	375	380
Leu Lys Thr Leu Ala Asp Phe Asp Pro Arg Val Ser Ile Arg Leu Pro		
385	390	395
Ser Thr Ser Gly Ser Glu Gly Val Pro Phe Arg Thr Val Ser Glu Trp		
	405	410
		415
Leu Glu Ser Ile Lys Met Gln Gln Tyr Thr Glu His Phe Met Ala Ala		
	420	425
		430
Gly Tyr Thr Ala Ile Glu Lys Val Val Gln Met Thr Asn Asp Asp Ile		
	435	440
		445
Lys Arg Ile Gly Val Arg Leu Pro Gly His Gln Lys Arg Ile Ala Tyr		
	450	455
		460
Ser Leu Leu Gly Leu Lys Asp Gln Val Asn Thr Val Gly Ile Pro Ile		
465	470	475
		480
Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu		
	485	490

<210> 43

<211> 9808

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion Protein Construct

<400> 43

ctttaaacgt ggatcatttt ctttaaattt atgctgacga cctttgaatt tgcctttttt	60
cttagcaatt tcgattcctt gtgctgacg ttccttaatt ttttttcgtt ctgattctgc	120
ttgatacttg tacaattcaa tgacaaggct attaatcaaa cgccttaaatt tttcatcttc	180
aataccattc attgagggta aatttaagac ttccagggtt gcccccttaa tttgaatttg	240
attcatcaat tctgttaatt ctttattatt tcgtcctaatt cgatctaatt cagtaacaat	300
aacaatatcc ccttcacgaa tatagttaag catagcttgt aattgtgggc gttcgaccga	360
ttgaccgctt aatttgctctg aaaagacctt agaaacgccc tgtaacgctt gtaattgccg	420
atctaagttc tgttctttgc tactgacacg tgcataacca atttttagcca ttttcaacca	480
acctctaaaa ttctctcggt tgcaataacc aatcagcaat atctactttt tcaatttcaa	540
attgcttatac agaaattgtc ttttcgtaag cgataaaatc ttgcgcatat tgttgctcat	600
taaaaatagc caccacttcg tcatttttcta aaactcgata aataaatttt ttcattttac	660
tcctcctatt atgccaact taaatgacct attcaccaag tcaattatac tgctaaaatc	720
atattaggac aaataggtat actctattga cctataaatg atagcaactt aaaagatcaa	780

gtgttcgctt cgctctcact gcccctcgac gttttagtag cctttccctc acttcggttca	840
gtccaagcca actaaaagtt ttcggggtac tctctccttc tccccctaat aattaattaa	900
aatcttactc tgtatatttc tgctaatacat tcactaaaca gcaaagaaaa acaaacacgt	960
atcatagata taaatgtaat ggcatagtgc gggtttttatt ttcagcctgt atcgtagcta	1020
aacaaatcga gttgtgggtc cgttttgggg cgttctgccca atttgtttag agtttcttga	1080
ataaatgtac gttctaaatt aaacgaagct gtcagcgcct ttatatagct ttctcgttct	1140
tcttttttta atttaatgat cgatagcaac aatgatttaa cactagcaag ttgaatgccca	1200
ccatttcttc ctggtttaaat cttaaagaaa atttcctgat tcgccttcag taccttcagc	1260
aatttatcta atgtccgttc aggaatgcct agcacttctc taatctcttt tttggtcgtc	1320
gctaaataag gcttgatac atcgcttttt tcgctaatat aagccattaa atcttctttc	1380
cattctgaca aatgaacacg ttgacgttcg cttctttttt tcttgaattt aaaccacct	1440
tgacggacaa ataaatcttt actggtaaaa tcacttgata cccaagcttt gcaaagaatg	1500
gtaatgtatt ccctattagc cccttgatag ttttctgaat aggcaattct aacaattttg	1560
attacttctt tttcttctaa gggttgatct aatcgattat taaactcaaa catattatat	1620
tcgcacgttt cgattgaata gcctgaacta aagtaggcta aagagagggg aaacataacg	1680
ctattgcgcc ctactaaacc cttttctcct gaaaatttcg tttcgtgcaa taagagatta	1740
aaccaggggt catctacttg tttttgcct tctgtaccgc ttaaaaccgt tagacttgaa	1800
cgagtaaagc ccttattatc tgtttgtttg aaagaccaat cttgccattc tttgaaagaa	1860
taacggtaat tgggatcaaa aaattctaca ttgtccgttc ttggtatacg agcaatccca	1920
aatgattgc acgttagatc aactggcaaa gactttccaa aatattctcg gatattttgc	1980
gagattatth tggctgcttt gacagattta aattctgatt ttgaagtcac atagactggc	2040
gtttctaaaa caaaatatgc ttgataacct ttatcagatt tgataattaa cgtaggcata	2100
aaacctaaat caatagctgt tgtaaaaata tcgcttgctg aaatagtttc tttttccgtg	2160
tgaatatcaa aatcaataaa gaaggtattg atttgtctta aattgttttc agaatgtcct	2220
ttagtgatg aacggttttc gtctgcatac gtaccataac gataaacgtt tgggtgtccaa	2280
tgcgtaaag tatcttgatt ttcgtgaatc gcttcttcgg aagtcagaac aacgccacgt	2340
ccgccaatca tgcttttttt tgagcgatac gcaaaaatag cccctttact tttacctggc	2400
ttggtagtga ttgagcgaat tttactatth ttaaatttgt actttaacaa gccgtcatga	2460
agcacagttt ctacaacaaa agggatatth attcagctgt tctcctttct tacgaaaatt	2520
aattagttag aagctacgat caaagttgaa tcacaacaaa aaaggcaatc aactaagttt	2580

ttcttaattg attgcctggt atcttcttaa agacttgaaa tcccctcaaa aacccgatat	2640
aatgggttta cagatattta agtatctgat taataaagta attaaatact ttaccaaatt	2700
ttgggtctcg acttctttta ttgattggtg gtaatcaatt aaggctcgca gttaaaattt	2760
ctcaggcttt aactggctcg ggctcttttt ttgtattctt tattcagttc gttgtttcgt	2820
tatatctagt atatcgcttt ttaaaaaaat aagcaatgat ttcgtgcatt attcacacga	2880
aatcattgct tttttcttct tccatttcta actccaatgt tacttgttct gtttctggtt	2940
ctgggtctgt tggctcattt gggattaaat ccactactag cgttgagtta gttccgtctc	3000
taatagccgg ttaagtaata gccggttaag tgggtcaaact ttgggaaaat ctcaaccgc	3060
attaagtttt gatgccatga caatcgttgg aaatttgaac aaaactaatg ctaaaaagct	3120
atctgacttt atgagtgtag agccacaaat acgactttgg gatatacttc aaacaaagtt	3180
taaagctaag gcacttcaag aaaaagttta tatcgaatat gacaaagtaa aagcagatac	3240
ttgggataga cgtaatatgc gtgttgaatt taatcccaat aaactcacac atgaagaaat	3300
gatttggtta aaacaaaata ttatcgacta catggaagat gacggtttta caagattaga	3360
cttagctttt gattttgaag atgatttgag cgattactat gcaatgactg ataaagcagt	3420
taagaaaact gttttttatg gtcgtaatgg caagccagaa acaaaatatt ttggtgtccg	3480
tgatagtgat agatttatta gaatttataa taaaaaaca gaacgtaaag ataacgcaga	3540
tgttgaagtt gtgtttgaac atttatggcg tgtagaagtt gaattaaaaa gagatatggt	3600
tgattactgg aatgattggt ttaatgattt acacatcttt gaaacctgcg tgggctactt	3660
tagaaaaaat taatgagcaa gctatggttt atactttgtt gcatgaagaa agtatgtggg	3720
gaaagctaag taagaatact aagactaaat ttaaaaaatt gattagagaa atatctcaa	3780
ttgattttaa ggaattaatg aaatcgactt taaaagcgaa cgaaaaaca ttgcaaaagc	3840
agattgattt ttggcaacgt gaatttaggt tttggaagta aaataagttt tatttgataa	3900
aaattgctaa ttcagtataa ttaatattta cgaggtgaca taacgtatga aaaaatcaga	3960
ggattattcc tcctaaatat aaaaatttaa aatttaggag gaagttatat atgactttta	4020
atattattga attagaaaat tgggatagaa aagaatattt tgaacactat tttaatcagc	4080
aaactactta tagcattact aaagaaattg atattacttt gtttaaagat atgataaaaa	4140
agaaaggata tgaaatttat ccctctttta tttatgcaat tatggaagtt gtaaataaaa	4200
ataaagtgtt tagaacagga attaatagtg agaataaatt aggttattgg gataagttaa	4260
atcctttgta tacagttttt aataagcaaa ctgaaaaatt tactaacatt tggactgaat	4320
ctgataaaaa cttcatttct tttataata attataaaaa tgacttgctt gaatataaag	4380
ataaagaaga aatgtttcct aaaaaaccga tacctgaaaa caccataccg atttcaatga	4440

ttccttggat	tgattttagt	tcatttaatt	taaatattgg	taacaatagc	agctttttat	4500
tgectattat	tacgataggt	aaattttata	gtgagaataa	taaaatttat	ataccagttg	4560
ctctgcaact	tcatcattct	gtatgtgatg	gttaccatgc	ttcactattt	atgaatgaat	4620
ttcaagatat	aattcatagg	gtagatgatt	ggatttagtt	tttagatttt	gaaagtgaat	4680
ttaattttat	acacgtaagt	gatcataaaa	tttatgaacg	tataacaacc	acattttttg	4740
gttgcttgtg	gttttgattt	tgaatttgg	tttgaactta	tggaactgatt	tattcagtcc	4800
attttttgtg	cttgcacaaa	aactagcctc	gcagagcaca	cgcattaatg	acttatgaaa	4860
cgtagtaaat	aagtctagt	tggtatactt	tacttggaag	atgcaccgaa	taaaaaatat	4920
tgaagaacaa	ctagcaaaa	attttaaaga	gttattttat	tttaagtctt	tataacatga	4980
gtgaagcgaa	tttttaaatt	tcgatagaaa	tttttacatc	aaaaagcccc	ctgtcaaaat	5040
tgacgaaggg	ggttttttgg	cgcacgcttt	tcgttagaaa	tatacaagat	tgaaaatcgt	5100
gtataagtgc	gccctttggt	ttgaacttag	cacgttacat	caatttttta	aatgatgta	5160
taagtgcgcc	cttttaaatt	ttgagtgatt	atattttttg	agttagaaaa	agggattggg	5220
aaaatttccc	aaaataattt	aaaaaataag	caaaaatttt	cgatagagaa	tgtgctattt	5280
tttgtcaaag	gtgtatacct	tgactgtgct	tgctgttaca	ttaagtttat	ttttaagtta	5340
ttaaaaaaga	aatagctttt	aaagtttggc	tcgctgtcgc	tttataaagc	tgattgactt	5400
ttgattgcaa	actacttaaa	gaaaacaaac	tcggactatt	cgttttcttc	tctttggttt	5460
gaacatcagc	aattatcccc	tcttgattgc	ctatttttagc	ttgttttagaa	gaaacaaaag	5520
ctaaaagctc	ctcttggggt	ttaaaacgct	gtgtggggct	tagaacgccc	ttaaacgacc	5580
cttggtttac	ttttatacta	gcttcacct	cgaaaaaagg	ttctttttta	aaattctcta	5640
tggtctcctg	gcgctgaaaa	aataaggtat	aagggtggcg	tttgaacacg	tcctagtga	5700
aatgtacctt	gtacgcccct	tctgttgtaa	atttaacgta	tacaaagggc	ttgcgttcac	5760
gccgatcaac	caatcggcaa	tttggcgtgt	ttgcgcttct	tgataaaagg	gatagtaatt	5820
cattccaggt	tgcaaatttt	gaaaaccgct	tcggattaca	tctttttcta	agctattgat	5880
ccatagtctt	ttaaagtgtt	tatcttttga	aaaggcattt	gctttatgga	taatcgacca	5940
ggcgatatatt	tcaccttctc	tgctgctatc	tgttgcaaca	ataattgtat	ttgccttttt	6000
gagaagttct	gcaacaattt	taaactgctt	tcccttatct	tttgcaactt	caaaatcgta	6060
tcgatcagga	aaaatcggca	aagattcaag	tttccaattt	tgccactttt	cgtcataatg	6120
acctggttct	gctaattcca	ctaaatgccc	aaaaccaaag	gtgataaacg	tttcatctgt	6180
aaatagtggg	tctttgatct	caaaataacc	gtcttttttg	gtgctttggt	ttaaagcact	6240

tgcgtaggct	aatgcctggc	ttggtttttc	agctaaaata	accgtactca	ttactatcc	6300
ctcttttcat	tgttttttct	ttgatcgact	gtcacgttat	atcttgctcg	ataccttcta	6360
aacgttcggc	gattgattcc	agtttggtct	tcaacttctt	tatcggataa	accattcaaa	6420
aacaaatcga	aagcatggat	gcgccgcgtg	cggctgctgg	agatggcgga	cgcgatggat	6480
atgtttctgcc	aagggttggg	ttgcgcattc	acagttctcc	gcaagaattg	attggctcca	6540
attcttgagg	tggatgaatcc	gttagcgagg	tgccgcgggc	ttcattcag	gtcgagggtg	6600
cccggctcca	tgcaccgcga	cgcaacgcgg	ggaggcagac	aaggatatagg	gcggcgccta	6660
caatccatgc	caaccggttc	catgtgctcg	ccgaggcggc	ataaatcgcc	gtgacgatca	6720
gcggctccagt	gatcgaagtt	aggctggtaa	gagccgcgag	cgatccttga	agctgtccct	6780
gatggctcgtc	atctacctgc	ctggacagca	tggcctgcaa	cgcgggcatc	ccgatgccgc	6840
cggaagcgag	aagaatcata	atggggaagg	ccatccagcc	tcgcgtcgca	atacgactca	6900
ctatagggcg	aattgggtac	cgggcccccc	ctcgaggctg	acggtatcga	taagcttgat	6960
atcgaattcc	tgcagcccgg	gggatccact	agttctagag	cggccgccac	cgcggtggag	7020
ctccagcttt	tgttcccttt	agtgagggtt	aatgctagaa	atattttatc	tgattaataa	7080
gatgatcttc	ttgagatcgt	tttggctctg	gcgtaatctc	ttgctctgaa	aacgaaaaaa	7140
ccgccttgca	gggcgggttt	tcgaagggtc	tctgagctac	caactctttg	aaccgaggta	7200
actggcttg	aggagcgcag	tcacaaaaac	ttgtcctttc	agtttagcct	taaccggcgc	7260
atgacttcaa	gactaactcc	tctaaatcaa	ttaccagtgg	ctgctgccag	tgggtgctttt	7320
gcatgtcttt	ccgggttgga	ctcaagacga	tagttaccgg	ataaggcgca	gcggtcggac	7380
tgaacggggg	gttcgtgcat	acagtccagc	ttggagcgaa	ctgcctaccc	ggaactgagt	7440
gtcaggcgtg	gaatgagaca	aacgcggcca	taacagcgga	atgacaccgg	taaaccgaaa	7500
ggcaggaaca	ggagagcgca	cgaggagacc	gccaggggga	aacgcctggg	atctttatag	7560
tectgtcggg	tttcgccacc	actgatttga	gcgtcagatt	tcgtgatgct	tgtcaggggg	7620
gcggagccta	tggaaaaacg	gctttgccgc	ggccctctca	cttccctggt	aagtatcttc	7680
ctggcatctt	ccaggaaatc	tccgccccgt	tcgtaagcca	tttccgctcg	ccgcagtcga	7740
acgaccgagc	gtagcgagtc	agtgagcgag	gaagcggaat	atatcctgta	tcacatattc	7800
tgctgacgca	ccggtgcagc	cttttttctc	ctgccacatg	aagcaattca	ctgacaccct	7860
catcagtgcc	aacatagtaa	gccagtatac	actccgctag	cgctgatgtc	cggcggtgct	7920
tttgccgtta	cgcaccaccc	cgtcagtagc	tgaacaggag	ggacagctga	tagaaacaga	7980
agccactgga	gcacctcaaa	aacaccatca	tacactaaat	cagtaagttg	gcagcatcac	8040
ccgacgcact	ttgcgccgaa	taaatacctg	tgacggaaga	tcacttcgca	gaataaataa	8100

atcctggtgt	ccctgttgat	accggaagc	cctgggcca	cttttggcga	aatgagacg	8160
ttgatcgga	cgtaagaggt	tccaactttc	accataatga	aataagatca	ctaccgggcg	8220
tattttttga	gttatcgaga	ttttcaggag	ctaaggaagc	taaaatggag	aaaaaatca	8280
ctggatatac	caccgttgat	atatcccaat	ggcatcgtaa	agaacatttt	gaggcatttc	8340
agtcagttgc	tcaatgtacc	tataaccaga	ccgttcagct	ggatattacg	gcctttttaa	8400
agaccgtaaa	gaaaaataag	cacaagtttt	atccggcctt	tattcacatt	cttgcccgcc	8460
tgatgaatgc	tcatccggaa	ttccgtatgg	caatgaaaga	cggtgagctg	gtgatatggg	8520
atagtgttca	cccttggtac	accgttttcc	atgagcaaac	tgaaacgttt	tcatcgctct	8580
ggagtgaata	ccacgacgat	ttccggcagt	ttctacacat	atattcgcaa	gatgtggcgt	8640
gttacgggtga	aaacctggcc	tatttcccta	aagggtttat	tgagaatatg	tttttcgtct	8700
cagccaatcc	ctgggtgagt	ttcaccagtt	ttgatttaaa	cgtggccaat	atggacaact	8760
tcttcgcccc	cgttttcacc	atgggcaaat	attatacgca	aggcgacaag	gtgctgatgc	8820
cgctggcgat	tcaggttcat	catgccgtct	gtgatggctt	ccatgtcggc	agaatgctta	8880
atgaattaca	acagtactgc	gatgagtggc	agggcggggc	gtaatttttt	taaggcagtt	8940
attggtgccc	ttaaacgcct	ggtgctacgc	ctgaataagt	gataataagc	ggatgaatgg	9000
cagaaattcg	aaagcaaatt	cgacccggtc	gtcggttcag	ggcagggtcg	ttaaatagcc	9060
gcttatgtct	attgctggtt	taccggttta	ttgactaccg	gaagcagtgt	gaccgtgtgc	9120
ttctcaaata	cctgaggcca	gtttgctcag	gctctccccg	tggaggtaat	aattgacgat	9180
atgatcattt	attctgcctc	ccagagcctg	ataaaaacgg	ttagcgcttc	gttaatacag	9240
atgtaggtgt	tccacagggg	agccagcagc	atcctgcgat	gcagatccgg	aacataatgg	9300
tgcagggcgc	ttgtttcggc	gtgggtatgg	tggcaggccc	cgtggccggg	ggactgttgg	9360
gcgctgccgg	cacctgtcct	acgagttgca	tgataaagaa	gacagtcata	agtgcggcga	9420
cgatagtcat	gccccgcgcc	caccggaagg	agctaccgga	cagcggtgcg	gactgttgta	9480
actcagaata	agaaatgagg	ccgctcatgg	cgttgactct	cagtcatagt	atcgtggtat	9540
caccggttgg	ttccactctc	tgttgcgggc	aacttcagca	gcacgtaggg	gacttccgcg	9600
tttcagact	ttacgaaaca	cggaaccga	agaccattca	tgttgttgct	caggctgcag	9660
acgttttgca	gcagcagtcg	cttcacgttc	gctcgcgtat	cggtgattca	ttctgctaac	9720
cagtaaggca	accccgccag	cctagccggg	tcctcaacga	caggagcacg	atcatgcgca	9780
cccgtggcca	ggacccaacg	ctgcccga				9808

<211> 26
 <212> PRT
 <213> *Listeria monocytogenes*
 <400> 44
 Met Lys Lys Ile Met Leu Val Phe Ile Thr Leu Ile Leu Val Ser Leu
 1 5 10 15
 Pro Ile Ala Gln Gln Thr Glu Ala Lys Asp
 20 25
 <210> 45
 <211> 59
 <212> PRT
 <213> *Listeria monocytogenes*
 <400> 45
 Met Thr Asp Lys Lys Ser Glu Asn Gln Thr Glu Lys Thr Glu Thr Lys
 1 5 10 15
 Glu Asn Lys Gly Met Thr Arg Arg Glu Met Leu Lys Leu Ser Ala Val
 20 25 30
 Ala Gly Thr Gly Ile Ala Val Gly Ala Thr Gly Leu Gly Thr Ile Leu
 35 40 45
 Asn Val Val Asp Gln Val Asp Lys Ala Leu Thr
 50 55
 <210> 46
 <211> 53
 <212> PRT
 <213> *Bacillus subtilus*
 <400> 46
 Met Ala Tyr Asp Ser Arg Phe Asp Glu Trp Val Gln Lys Leu Lys Glu
 1 5 10 15
 Glu Ser Phe Gln Asn Asn Thr Phe Asp Arg Arg Lys Phe Ile Gln Gly
 20 25 30
 Ala Gly Lys Ile Ala Gly Leu Ser Leu Gly Leu Thr Ile Ala Gln Ser
 35 40 45
 Val Gly Ala Phe Gly
 50
 <210> 47
 <211> 21
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: Primer
 <400> 47

gtcaaaacat acgctcttat c 21

<210> 48
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 48
 acataatcag tccaaagtag atgc 24

<210> 49
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 49
 ctctggtacc tcctttgatt agtatattc 29

<210> 50
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 50
 ctctggatcc atccgcgtgt ttcttttcg 29

<210> 51
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Epitope insert

<400> 51
 gattataaag atgatgatga taaa 24

<210> 52
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Epitope

<400> 52

Asp Tyr Lys Asp Asp Asp Asp Lys
1 5

<210> 53
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Epitope insert

<400> 53
gaacaaaaat taattagtga agaagattta

30

<210> 54
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Epitope

<400> 54

Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu
1 5 10

<210> 55
<211> 9
<212> PRT
<213> Mus sp.

<400> 55

Ser Pro Ser Tyr Val Tyr His Gln Phe
1 5

<210> 56
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Epitope

<400> 56

Ser Pro Ser Tyr Ala Tyr His Gln Phe
1 5

<210> 57
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

 <400> 57
 ctctggtacc tcctttgatt agtatattc 29

 <210> 58
 <211> 36
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Primer

 <400> 58
 caatggatcc ctcgagatca taatttactt catccc 36

 <210> 59
 <211> 32
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Primer

 <400> 59
 atttctcgag tccatggggg gttctcatca tc 32

 <210> 60
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Primer

 <400> 60
 ggtgctcgag tgcggccgca agctt 25

 <210> 61
 <211> 37
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Primer

 <400> 61
 cgattcccct agttatgttt accaccaatt tgctgca 37

 <210> 62
 <211> 31
 <212> DNA
 <213> Artificial Sequence

 <220>

<223> Description of Artificial Sequence: Primer

<400> 62
gcaaattggt ggtaaacata actaggggaa t 31

<210> 63
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Epitope insert

<400> 63
agtcgaagtt atgcatatca tcaattt 27

<210> 64
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 64
cgatagtcca agttatgcat atcatcaatt tgc 33

<210> 65
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 65
gtcgcaaatt gatgatatgc ataacttgga ctat 34

<210> 66
<211> 8
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Consensus Sequence

<220>
<221> misc_feature
<222> (1)..(1)
<223> n is a, c, g, or u

<400> 66
naggaggu 8

<210> 67
 <211> 19
 <212> DNA
 <213> *Listeria monocytogenes*

<400> 67
 aaggagagtg aaacccatg 19

<210> 68
 <211> 240
 <212> DNA
 <213> *Listeria monocytogenes*

<400> 68
 ggtacctcct ttgattagta tttcctatc ttaaagtac ttttatgttg aggcattaac 60
 atttggttaac gacgataaag ggacagcagg actagaataa agctataaag caagcatata 120
 atattgcggt tcatcttttag aagcgaattt cgccaatatt ataattatca aaagagaggg 180
 gtggcaaacg gtatttggca ttattaggtt aaaaaatgta gaaggagagt gaaacccatg 240

<210> 69
 <211> 240
 <212> DNA
 <213> *Listeria monocytogenes*

<400> 69
 ggtacctcct ttgattagta tttcctatc ttaaagttac ttttatgttg aggcattaac 60
 atttggttaat gacgtcaaaa ggatagcaag actagaataa agctataaag caagcatata 120
 atattgcggt tcatcttttag aagcgaattt cgccaatatt ataattatca aaagagaggg 180
 gtggcaaacg gtatttggca ttattaggtt aaaaaatgta gaaggagagt gaaacccatg 240

<210> 70
 <211> 5
 <212> PRT
 <213> *Listeria monocytogenes*

<400> 70
 Thr Glu Ala Lys Asp
 1 5

<210> 71
 <211> 5
 <212> PRT
 <213> *Listeria monocytogenes*

<400> 71
 Asp Lys Ala Leu Thr
 1 5

<210> 72
<211> 5
<212> PRT
<213> Bacillus subtilis

<400> 72

Val Gly Ala Phe Gly
1 5